

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:41:32 ; Search time 34.65 Seconds
(without alignments)
1600.893 Million cell updates/second

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSSFQSCQIISLIFTFAV RSYPEILTLKTYLHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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A_Geneseq_0601:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IMMEDIATE

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	915	17 AAR86596	A2058 autotaxin pr
2	5019	100.0	915	22 AAY71987	Human melanoma aut
3	4681	93.3	863	22 AAY71988	Human teratocarcin
4	4632	92.3	859	22 AAY71991	Human autotaxin pr
5	4533	90.3	829	17 AAR86578	Autotaxin derived
6	4430.5	88.3	858	22 AAY71997	Rat autotaxin vari
7	4430.5	88.3	858	22 AAY71999	Rat autotaxin vari
8	4429.5	88.3	858	22 AAY71998	Rat autotaxin vari
9	4426.5	88.2	858	22 AAY71986	Rat autotaxin prot
10	4423.5	88.1	858	22 AAY71996	Rat autotaxin vari
11	4422.5	88.1	858	22 AAY71995	Rat autotaxin vari

12	4341	86.5	AAR86595
13	4306	85.8	AYY71989
14	4279	85.3	AAR86580
15	3842	76.5	AAR86579
16	1955.5	39.0	AYY83620
17	1955.5	39.0	AAR79148
18	1955.5	39.0	AYY39355
19	1955.5	39.0	AAB00195
20	1954.5	38.9	AYY83621
21	646.5	12.9	AAG31321
22	609	12.1	AAG29474
23	609	12.1	AAG29473
24	599	11.9	400
25	569	11.3	359
26	512	10.2	453
27	512	10.2	453
28	512	10.2	453
29	484	9.6	338
30	467	9.3	440
31	465.5	9.3	477
32	465.5	9.3	477
33	465.5	9.3	477
34	465	9.3	411
35	465	9.3	428
36	360	7.2	438
37	357	7.1	355
38	357	7.1	355
39	241.5	4.8	133.
40	200	4.0	92
41	179	3.6	109
42	141	2.8	39
43	134	2.7	111
44	134	2.7	182
45	134	2.7	452
			16 AAR80041

RESULT 1
AAR86596
ID AAR86596 standard; Protein; 915 AA.
XX
AC AAR86596;
XX
DT 01-JUL-1996 (first entry)
XX
DE A2058 autotaxin protein.
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.

Ward, John

XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
 CC sequence represents the full length protein sequence of the A2058
 CC melanoma cell line ATX protein. ATX is an autocrine motility
 CC stimulating protein which is present in cancer cells. ATX stimulates
 CC both random and directed migration of melanoma cells. The tumourous form
 CC of ATX is a secreted protein, while the transmembrane bound form is not
 CC present in tumour cells. The cDNA encoding this sequence can be used in
 CC a vector, to transform cells. The recombinant cells can then be used to
 CC produce the peptide sequences. Antibodies specific for these sequences
 CC can be produced, and can be used in cancer diagnosis and therapy.
 CC Different sites of localisation of the protein are utilised for diagnosis
 CC and prognosis of the stages of tumour progression. The sequences can be
 CC used in treatment methods to advantageously block the activity of the
 CC secreted form of ATX, while having little effect on the membrane form of
 CC ATX.

XX SQ Sequence 915 AA;

Query Match 100.0%; Score 5019; DB 17; Length 915;
 Best Local Similarity 100.0%; Ered. No. 0;
 Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MARRSSFQSCQIISLRLFTFAVGVSICLGLFTAHRIKRAEGWEGPPTVLSDSPWTNISGSKC 60
 Db 1 marrssfqscqislfavgsiclgftahrikraegwegpptvlsdspwtnisgskc 60
 QY 61 GRCFELQEAGPPDCCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNNEENACHC 120
 Db 61 grcfelqeagppdccrcdnlcksytsccchdfdelclktargwectkdrgevrneenachc 120
 QY 121 SEDCLARGDCCTNYQVVCKGE SHWVDDCEEIKAAECPAGFVRPPLIIFSVDGFRAS YMK 180
 Db 121 sedclargdcctnyqvvckgeshwvddceeeikaaecpafvrppliifsvdgfrasymk 180
 QY 181 KGSKVM P NIEKLRS CGTHSPYMRPVYPTKTFPNLYTLATLGYPESH GIVGNSM YDPV F D A 240
 Db 181 kgskvm p nieklrs cgthspymrvpyptktfpnlytlatlgypeshgivgnsmydpv f da 240
 QY 241 TPHLRGREKFNHRWGGQPLWITATKQGVKAGTFFWSSVIPHERRILITLRLWLTPDHER 300
 Db 241 tphlrgrrekfnhrwggqplwitatqgvkagtf f wssvipherrilittlrlwltpdher 300
 QY 301 PSVYAFYSEQOPDFSGHKYGPFGPEESSYYGS PFTPAKRPKRQERPVAPPKKRRR 360
 Db 301 psvyafyseqopdfsghk ygpfgpeessyygs pftpakrpkrqerpvappkkrrr 360
 QY 361 KIH RMDH YAAETRODKMTNPLREIDTKIVGQLMDGLKQLKLRRCVNVTFYGDHG MEDVPCD 420
 Db 361 kihrm dh yaaetrqdkmtnplreidtkivgqlmdglkq1k1rrcvnvifvgdhgmedvtd 420
 QY 421 RTEFLSNYLTVDDITLVPGTLGRIRS KFSNNNAKYDPKAIIANLTCKPDQHF KPYLKQH 480
 Db 421 rteflsnyltvdditlvpgtlgrirsksf snnnak ydpkaiianltckpdqhf kpylkqh 480
 QY 481 LPKRLHYANRRIEDIHLVERRW HARKPLDWYKKPSKGCKCFQGDHFDNKVN SMQTVF 540
 Db 481 lpkrlyanrriedi hllverrw harkpldw ykkpskgckcfqgdhqfdnkvn smqtvf 540
 QY 541 VGYGPTFKYKTKVPPFENI ELYNVMCDLGLKPA PNNNGTHGSLNHLRLRTNTFRPTMPEEV 600
 Db 541 vgygptfk yk tkvppf enielynmcdlglkpa pnnngthgslnhlrlrtntfrptmpeev 600
 QY 601 TRPNYPGIMYLQSDEFDLGCT CDDKVEPKNKLDELNKR LHTKGSTEERHLLYGRPAVLYRT 660
 Db 601 trpnypgimylqsdefdlgct cddkvepknklde lnkr lhtkgst eerhll ygrpavlyrt 660
 QY 661 RYDILYHTDFESGYSEIIFMLLIWTSVSKQAEVSSVPDH LTSCVRPDV RVSPSFQNCL 720
 Db 661 rydil yhtdfesgyseifmllwtsvskqaevssvpdh ltscvrpdv rvspsfsqnc1 720
 QY 721 AKNDKQMSYGGFLFPYLLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLVKKYASER 780

XX SQ Sequence 915 AA;

RESULT 2
 ID AAY71987 standard; Protein; 915 AA.

XX XX
 XX AC
 XX DT 28-MAR-2001 (first entry)

XX DE Human melanoma autotaxin.

XX KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; melanoma.

XX KW Homo sapiens.

XX FH Location/Qualifiers
 FT Binding-site 127..129
 FT /label= RG D_binding_domain
 FT Active-site 201..213
 FT /note= "Autotaxin phosphodiesterase catalytic site"

XX PN WO2000068386-A1.

XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12402.

XX PR 07-MAY-1999; 99US-0306979.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kelly JD;

XX DR WPI; 2001-007397/01.

XX PT New autotaxin Proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX PS Claim 27; Page 105-108; 126pp; English.

XX CC The present sequence is autotaxin isolated from human melanoma cells. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities.

CC Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).

Transgenic animals that overexpress autotaxin are models for human metabolic diseases.

RESULT 3							
	AAY71988	ID	AY71988 standard	Protein	863 AA.		
X	Sequence 915 AA;						
Q	Query Match 100.0%; Score 5019; DB 22; Length 915;	Best Local Similarity 100.0%; Pred. No. 0;	Mismatches 0; Indels 0;	Gaps 0;			
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Y	1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60						
b	1 marrssfqscqisiiftfavgvsiclgftahrikragegpptvlspwtnisgsck 60						
Y	61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDDELCLKTARGWECTKDRCGEVRNEENACHC 120						
b	61 grcfelqeagppdcrcdnicksytsccchdfdelclktargwectkdrgevrneenachc 120						
Y	121 SEDCLARGDCCCTNYQVVCKGESHWDDCEEIKAAECPAGEFVRPPLIIFSVDGFRASYMK 180						
b	121 sedclargdcctnyqvckgeshwdddeeikaacpagfvrrpliifsvdgfrasymk 180						
Y	181 KGSKVMPNIEKLRSRGTHSPYMPVYPTKTEPNLYTLATGLYPESHGIVGNNSMYPDPVFDA 240						
b	181 kgskvmpnikeklrsrgthspsymrvpyptktpnlytlatglypeshgivgnsmypdpvfda 240						
Y	241 TFHLRGREKFNFHWWGGQPLWITATKQGVKAGTFFFWSVVIPHERILTLRWLTLPDHER 300						
b	241 tfhlrgrekfnhwwggqplwitatkgvkaqtffwsvvipherriltilrwltlpdher 300						
Y	301 PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPEFTPAKRPKRKVAPKRQRERPVAPPKKRR 360						
b	301 psvyafyseqpdfsghkkygpf9peessygspeftpaakrpkrkvapkrqrerpvappkkrrr 360						
Y	361 KIHRMDHYAAETRQDKMTNPRLREIDKIVGQLMDGLKQLRRRCVNVIFVGDHGMEDVTCD 420						
b	361 kihrmddyaaetrqdkmtnpireidkivgqlmdgikqlkq1lrrrcvnvifvgdhgmedvtcd 420						
Y	421 RTEFLSNYLTVPGTLGRIRSKESENNAKYDPKAIIANLTCKKPKDQHFKPYLKQH 480						
b	421 rteflsnyltvpgtlgrirsksfssnnakydpkaiianltckkpkdqhfkpylkqh 480						
Y	481 LPKRLHYANNRRIEDIHLLVERRWHARKPLDVKYKKPSKGKCFQGDHGFDNRKVNNSMQTVF 540						
b	481 lpkrlhyannrriedihllverrwharkpldvykkpsgkcfqgdhgfdkvnsmqtvf 540						
Y	541 VGYGPTFKYTKVPPFENIELNYVMCDLLGLKPAPNNNGTHGSLNHILLRTNTFRPTMPEEV 600						
b	541 vgygptfktykvpfenielnyvmcdllglkpapnnngthslnhllrtntfrptmpeev 600						
Y	601 TRPNYPGIMYLQSDFDLGCCTCDDKVEPKNKLDLENKRLHTKGSTEERHLLYGRPAVLYRT 660						
b	601 trpnypgimylqsdfdl9ctcdkvepknkldlenkrlhtkgsteerhlygrpavlyrt 660						
Y	661 RYDILYHTDFESGYSEEIFMLLWTSYTYSVKQAEVSSVPDHLTSCVRPDVRVSPSFQNCL 720						
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Y	721 AYKNDKOMSYGFLFPPLSSSPEAKYDAFLVLTNMVPMYPAFKRVWNMFQRLVKKYASER 780						
b	721 aykndkqmsygflfpplyssspeakydaflvtnmvpmypafkrvwnyfqrvlvkkyaser 780						
Y	781 NGVNVISGPIFDDYDGLHDTEDKIKQYVEGSSIPVPTHYSIIITSCLDFTQPADKCDGP 840						
b	781 ngnvisgpiifddydglhdtedkikqyvegssipvpthysiiitscldftqpdkcdgp 840						
Y	841 LSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 900						
b	841 lsvssfilphrpdneescnssdeskwveelmkmhtarvrdiehltsldffrktsrsype 900						
Y	901 ILTLLKTYLHTYESEI 915						
b	901 iltllktylhtyesei 915						

QY	61	GRCELEQEAEGPPDCRCDDNLCKSYTSCCHDFDELCLKTAGWECTKDRCGEVRNNEENACHC	120	KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
Db	61	grcfelqeagppdcrcddnlcksytsccchdfdelclktarawectkdrgevrneenachc	120	KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
QY	121	SEDCLEARDCCTNYQVVCCKGE SHWVDDCEEEIAECPAGFVRPPLIIFSVDGFRAS YMK	180	KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
Db	121	sedclargdcctnqyvvcckgeshwvddceeeiaaecpafvrpplifsvdgfrasymk	180	KW ATPase; adenosine-5'-triphosphatase activity.
QY	181	KGSK VMPNIEKL RSLSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGTIVGNMSYDPVFD A	240	XX Homo sapiens.
Db	181	kgsk vmpniekl rslscgthspymrpyptkfpnlytlatglypeshgtivgnsmypvfd a	240	XX Key
QY	241	TFHILRGREKFNHRWWGGQPLWITATKGVKAGTFEWSSVVI PHERRILTILRWLTLPDHER	300	XX Domain
Db	241	tfhilrgrekfnhrwwggqplwitatkgvkagtfewssvvipherrliltqlwtlpdher	300	XX FT /note= "putative transmembrane domain"
QY	301	PSVYAFYSEQPQDFSGHKYGPFGPEESSYGS PFTPAKRPKR KQERPVAPPKRRR	360	XX FT Cleavage-site
Db	301	psv yafyseqpd fsghk ygpfgpe-----	324	XX FT Binding-site
QY	361	KIHRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNNTFVG D HGMEDVTC D	420	XX FT Active-site
Db	325	-----mtnprieidkivgq lmdglkq1k1hrcvnvi fvgd hgm edv tcd	368	XX FT /label= RGD_binding_domain
QY	421	RTEEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKA YDPKA IANL TCKKP DQHFKP YLKQH	480	XX FT /note= "putative phosphodiesterase active site"
Db	369	rteeflsnyltnvdditlvpgt lgrirskfsnnakaydpkai anl tckkp d qhfk p ylkqh	428	XX PN WO200068386-A1.
QY	481	LPKRLHYANNRRIEDIHLLVERRW HARKPLDVKKLKPAPNNGTHGSLNHL RRTNTFRPTM PBEV	540	XX PD 16 -NOV-2000.
Db	429	1pkrlhyannrriedihllverrw harkpldvkkp d qhfk p ylkqh	488	XX PF 05-MAY-2000; 20000WO-US12402.
QY	541	VGYGPTFKYKTKVPPFENI ELYNVMCDLLGLKPA P NNGTHGSLNHL RRTNTFRPTM PBEV	600	XX PR 07-MAY-1999; 99US-0306979.
Db	489	vgygptfk yktpfen ielynmcdllk p apnngthgslnhl rrtntfrptmpeev	548	XX PA (ZYMO) ZYMOGENETICS INC.
QY	601	TRPNYPGIMYLQSDFDLGCT CDDKVEPKNKLD E LNKL RLHTKGSTEERHLLYGRPAVLY RT	660	XX PA Kelly JD;
Db	549	trprypgimylqsdfdlqctcdkvepknkldelnkrlhtkgsteerhll ygrpavly rt	608	XX PI
QY	661	RYDILYHTDFESGYSEIFMLLWT SYTVSK QAEVSSVPDH LTSCVRP DPVSPSFQNCL	720	XX WPI; 2001-007397/01.
Db	609	rydillyhtdfesgyseifmlp wtsytvsk qaevssvpdh ltscvrp dpvspfsqncl	668	XX DR N-PSDB; AAD02133.
QY	721	AYKNDKQMSYGFLLFPYLISSPEAKYDAFLV TNMVPMPYPAFKRVWN YFORVLVKKYASER	780	XX DR
Db	669	aykn dkqmsygfllfppylsspeakydaflvtnmpmpy pafkrvwnyfrgrvlvkk yaser	728	XX DR
QY	781	NGVNVISGP IFDYD YDGLHD TEDKIKOYVEGSSIPVPTHYSIITSCLDFTQPADKCDGP	840	XX DR
Db	729	ngvnvisgp ifdyd ydglhd tedkikqyvegssipvpthysiitscl dftqp adkcdgp	788	XX DR
QY	841	L SVSS FILPHRPDNEECSSEDES KWEELMKMHTARV RDIEHLTS LUDFFRKTSRSY PE	900	XX DR
Db	789	l svss filphrp dneescs sedeskweelmk mhtarv rdiehlts ldf frktsrsy pe	848	XX DR
QY	901	IITLKTYLHTYESEI	915	Query Match 92.3%; Score 4632; DB 22; Length 859;
Db	849	iitl ktylhtyesei	863	Best Local Similarity 93.7%; Pred. No. 0; Mismatches 3; Gaps 1;
RESULT	4			
ID	AY71991	standard; Protein; 859 AA.		
XX				
AC	AY71991;			
XX				
DT	28-MAR-2001	(first entry)		
XX				
DE		Human autotaxin protein.		
XX				
KW		Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;		
KW				

Db	187	klrcsgthspymrvptkfpnlylatgypeshgivqnsmydpvfdatfhlgrekf	246	PR 25-MAY-1994; 94US-0249182.
QY	251	NHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTLRWLTLPHERPSVYAFYSEQ	310	XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
Db	247	nhrwwggqplwitatkkqgvkagtffwsvvipherrilqlqwtlpherpsvyaafyseq	306	XX PA
QY	311	PDFSGHKYKGPFGEESYYGSPFPTPAKPKRKVAPKRKRQERPVAPPKKRRKTHRMDHYAA	370	XX PI Krutzsch, Liotta L, Murata J, Schiffmann E, Stracke M;
Db	307	pdfsghkkygpfgepe-----	320	XX DR WPI; 1996-020533/02.
Db	371	ETRQDKMTNPRLREIDKIVGQLKLQLRRCVNVIIFVGDHGMEDVTCDRTEFLSNYLTT	430	XX DR Autotaxin motility stimulating protein, and DNA encoding it - used in cancer diagnosis and therapy
Db	321	-----mtnpnlreidkivq1md1qk1hrcvnvfvgdhwmedvtcdrteflsnylt	374	XX PT PT in cancer diagnosis and therapy
QY	431	NVDDITLVPGTGLGRIRSKFSNNAKYDPKAIIANLTCKKPQHFKPYLKQHLPKRLHYANN	490	XX PS Claim 4; Page 57-60; 112pp; English.
Db	375	nvdditlvpgtgrskfsnnakydpkaiianltckkpqhfkpylkqhlpkrlhyann	434	XX XX
QY	491	RRIEDIHLLYVERRWHAARKPLDVKKPSGKCFQGDHGFDNKVNNSMQTIVFVGYPFTFKYK	550	CC ANR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourous form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of ATX, while having little effect on the membrane form of ATX, while
Db	435	rriedihllyverrwhaarkpldvykkpsgkcfqgdhgfanckvnsmqtivfygygptfkyk	494	CC CC
QY	551	TKVPPFENIELINYVMCDLGLKPKAPNNNGTHGSILNHLLRTNTFRPTMPEEVTRPNYPGIMY	610	CC CC
Db	495	tkvppfenielynvmcdlglkpkapnnngthgsilhllrtntfrptmpeevtrpnypgimy	554	CC CC
QY	611	LQSDFDLGCTCDDKVEPKNKLDELNKLHKTGSTEEERHLLYGRPAVLTRYDILYHTDF	670	CC CC
Db	555	lqsdfdlgctcdkvepknkldelnkrhktgsteeerhlliygrpavlytrydilyhtdf	614	CC SQ Sequence 829 AA;
QY	671	ESGYSEIFLMLLWTSTYTSKQAEVSVPDVRVSPSCVRPDVRLTSCVRPDKHLSQNLCLAYKNDKQMSY	730	Query Match 90.3%; Score 4533; DB 17; Length 829;
Db	615	esgyseiflmlp1wtstvskqaevssvpdhltscvrpdrvspsfsqnclaykndkqmsy	674	Best Local Similarity 99.9%; Pred. No. 0; Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	731	GFLFPYPLSSSPEAKYDAFLVNTNMVPMPYPAFKRVWNFYQRLVYKKAESERNGVNVISGPI	790	QY 87 CHDFDELCLIKTARGWECTKDRBCGEVRENEENACHCSEDCLARGDCCTNYQVVKGEESHWD 146
Db	675	gfifppylssspeakydaf1vtnmpyafkrrwnyfqrvlvkkyaserngvnvisgpi	734	Db 1 chdfdelcliktaargwectkdrbcgevreenachcsedclargdcctnyqvckgeshwvd 60
QY	791	FDDYDGHLHDTEDKIKQYVEGSSSIYPVPTHYSIITSCLDFTQPADKCDGPLSVSSFSILPH	850	QY 147 DDCEEIKAECAPAGFVRPPLIIFSVDFRASYMKKGSKVMPNIEKLRSCTGHSPYMRPVY 206
Db	735	fddydghdtedkikqyvegsssiypvpthysiitscldf tqpadkcdgplsvssfilph	794	Db 61 ddceiikaecapagfvrppliifsvdfrasymkkgskvmpniesklrsctghspymrvy 120
QY	851	RPDNEECSNSSEDESKEWVEELMMKHTARVRDIEHLTLSDFERKTSRSYPEILTLKTYLHT	910	QY 207 PRKTFPMLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKFNHRWGGQPLWITATK 266
Db	795	rpdeeescnssedeskewveelmmkhtarvrdiehltsdffrktstsrsypeiltktylht	854	Db 121 ptktfpnlylatgypeshgivgnsmydpvfdatfhlgrekfnhrwgqqlwitatk 180
QY	911	YESEI 915	QY 267 QGVKAGTFFWSVVIPIHERRILTLRWLTLPLDHERPSVYAFYSEQPDFSGHKYGPGEES 326	
Db	855	yesei 859	Db 181 qgvkagttffwsvvipherritlrlwltlpdherpsvaya fyseqpdfsghkkygpqfgees 240	
RESULT	5		QY 327 SYGSPFTPAKRPKRQEROERPVAAPPKKRRKTHRMDHYAAETRQDKMTNPLREIDK 386	
AAR86578	ID	AAR86578 standard; Protein: 829 AA.	Db 241 sygspftpakrpkrqeroerpvaappkkrrkthrmhyaaetrqdkmtnplreidk 300	
XX	XX		QY 387 IVGQLMDGLKQLKLRRRCVNVIIFVGDFDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTGIR 446	
DT	28-JUN-1996	(first entry)	Db 301 ivgqlmdglkqlkrrcvnviifvgdhgmedvtcdrteflsnyltnvdditlvpgtgir 360	
XX	XX	Autotaxin derived from melanoma cell line A2058.	QY 447 SKFSNNAKYDPKAIIANLTCKKPQHFKPYLKQHLPKRLHYANNRRIEDIHLVERRHWV 506	
XX	XX	Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF; melanoma cell; tumour; antibody; cancer diagnosis; therapy.	Db 361 skfsnnakydpkaianltckkpqhfkpylkqhlpkrlhyanrrriedihiilverhwv 420	
OS	OS	Homo sapiens.	QY 507 ARKPLDVYKKPSGKCFQGDHGFDNKVNNSMOTVFGPYGPTFKYKTKVPPFENIELYNVMC 566	
XX	XX	W09532221-A2.	Db 421 arkpldvyykkpsgkcfqgdhgnvsmqtvfygygptfkycdkvtpfenielyvmc 480	
PN	PN		QY 567 DLLGLKPAPNNGTHGSLNHLRLRTNTFRPTMPEEVTRPNYPGIMYLOQSDFDLGCTCDKVE 626	
XX	XX		Db 481 d11qlkcapnngthgslnhllrtntfrptmpeevtrpnypgimy1qsddd1gctcdkve 540	
PF	PF	24-MAY-1995; 95WO-US06613.	QY 627 PKNKLDDELNRKRLBTRKGSTEERHLLYGRPAVLTRYDILYHTDFESGYSEIFMLLWTSY 686	
PR	PR	28-NOV-1994; 94US-0346455.	QY 627 PKNKLDDELNRKRLBTRKGSTEERHLLYGRPAVLTRYDILYHTDFESGYSEIFMLLWTSY 686	

Db	541	pknkidelnkrlhtkgsteerhlygrpavlyrtrydilyntdfesqyseifmlnlwtsy	600	CC with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotoxin are models for human metabolic diseases.
QY	687	TVSKQAEVSSVPDHLTSCVRPSPFSQNCLAYKNDKQMSYGFLEPPYLSSSPEAKY	746	CC Note: The present sequence is not shown in the specification but is derived from rat autotoxin protein sequence found in page 101-104 of sequence listing (AAV71986).
Db	601	tvsqqaevssvpdhltsqrpsfsqnclaykndkqmsygfleppylssspeaky	660	CC
QY	747	DAFLVTNMVPMYPAFKRVWNYFQRVLVKYASERNGVNVISGPIFDYDGHLHDTEDKIK	806	CC
Db	661	daflvtnmvpmypafkrwvnyfqrvlvkkyaserngvnvisgpfidydg1hdtedkik	720	CC
QY	807	QYVEGSSIPVPTHYSITTSCLDFTQPADKCDGPLSVSSFILPHRPDNNEESCNSSEDESK	866	XX Sequence 858 AA;
Db	721	qyegssipvpthysittscldftqpdakcdqplsvssfilsphrdneescnssedesk	780	XX
QY	867	WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESEI	915	Query Match 88.38; Score 4430.5; DB 22; Length 858;
Db	781	wveelmkmhtarvrdiehltlfrkttsrsypeiltkylhtyesei	829	Best Local Similarity 88.7%; Pred. No. 0; Mismatches 19; Indels 53; Gaps 2;
RESULT	6			Matches 803; Conservative 30; Gaps 2;
ID	AY71997	standard; Protein; 858 AA.		
XX	AY71997;			
XX				
DT	28-MAR-2001	(first entry)		
XX				
DE	Rat autotoxin variant (S236T).			
XX				
KW	autotoxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP Pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.			
XX				
DE	Rattus sp.			
OS	Synthetic.			
XX				
FH	Key Location/Qualifiers			
FT	Misc-difference 236			
FT	/note= "Wild type Ser substituted by Thr"			
XX				
PN	WO2000068386-A1.			
XX				
PD	16-NOV-2000.			
XX				
PF	05-MAY-2000; 2000WO-US12402.			
XX				
PR	07-MAY-1999; 99US-0306979.			
XX				
PA	(ZYMO) ZYMOGENETICS INC.			
XX				
PI	Kelly JD;			
XX				
DR	WPI; 2001-007397/01.			
XX				
PT	New autotoxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -			
XX				
PS	Disclosure; Page -; 126pp; English.			
XX				
CC	The present sequence is variant (S236T) of rat autotoxin protein.			
CC	Autotoxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.			
CC	Autotoxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotoxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated			
Db	734 fdyngd1rdtedekqyvegssipvpthysitstscldeftopadkcdgplsvssfilph	850		
QY	791 FDYDYGGLHDTEDKIKQYVEGSSIPVPTHYSITSTSCLDEFTOPADKCDGPLSVSSFILPH	910		
Db	734 fdyngd1rdtedekqyvegssipvpthysitstscldeftopadkcdgplsvssfilph	793		
QY	851 RPDNEESCNSEDESKEWELMKMHTARVRDIEHLSLDEFERKTTSRSYPEEILTLKTYLHT	910		
Db	794 rpndescnssedeskwveelmkmtarvrdiehltgdfrktsrsyseilktlyht	853		

XX	Rat autotoxin variant (R265K).	QY	191 KLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKF 250
DE		Db	186 kirscgthapymrvptktfpnlytlatglypeshivgnsmypydfdasfhlgrekf 245
KW	Rat; autotoxin; lipolysis; gluconeogenesis; insulin sensitivity;		
KW	adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;		
KW	therapy; metabolic disease; obesity; dyslipidemia; serum glucose;		
KW	non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;		
KW	type I phosphodiesterase activity; ATP Pyrophosphatase activity;		
KW	ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.		
XX	Rattus sp.	OS	319
OS	Synthetic.	OS	
XX			
FH	Key Location/Qualifiers	QY	371 ETRODKMTNPRLREIDKIVGQLMDGLKQLKLRRCCVNIVFVGDHGMEDVTCDRTEFLSNYLTT 430
FT	Misc-difference 265	Db	320 ----mtnpnlreidktvq1mdglkqlrlhrcvnvifvgdhgmtdrteflsnylt 373
FT	/note= "Wild type Arg substituted by Lys"	QY	431 NVDDITLVPGTGLRIRSKFSNNAKYDPRAIANLTCKKPQLKQHLPKRLHYANN 490
XX	WO200068386-A1.	Db	374 nvdditlvpgtlgriraksinnskydpktianltckkpqlkphpkrlhyann 433
XX	16-NOV-2000.	QY	491 RRIEDTHLLVERRWVHARKPLDVYKKPSGKCFQGDHGFDNKVNSMOTVFEVGYGPTFKYK '550
PD	05-MAY-2000; 2000WO-US12402.	Db	434 rriedihllvdrwvharkpldvyykkpsgkcfqgdhgfrankvnsmtvfvgygptfkry 493
XX	07-MAY-1999; 99US-0306979.	QY	551 TKVPPFENIELYNVMCDLLGLKPKAPNNGTHGSLNLHLLRTNTFRPTMPPEEVTRPNYPGIMY 610
PR	XX (ZYMO) ZYMOGENETICS INC.	Db	494 tkvppfenielyvmcdllglkpkapnnqthgsinhllrlrtntfrptmpdevsrpnypgimy 553
PA		QY	611 LQSDFDLGLCTCDKVEPKNKLDELNKRLHTKGSTEERHLLYGRPAVLRYTRDILYHTDF 670
PI	Kelly JD;	Db	554 lqsefdlgctcdkvepkknkleelnkrhkgsteerhlygrpavlyrtsdilyhtdf 613
XX	WPI; 2001-007397/01.	Db	614 esgyseifimplwtstiskqaevssipehltnccrvprdpvrvspgsqncldqmsy 673
DR		QY	731 GFLFPYLISSSPPEAKYDAFLVLTNVMVPMYPAFKRVWNYFQRVLVKKAYSERNGVNVISGPI 790
XX	New autotoxin proteins, useful e.g. for treating diabetes mellitus and	Db	674 gflfpyp1sssppeakydaf1vtnmvpmypafkrvwayfqrvlvkkyaserngvnvisgpi 733
PT	PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -	QY	791 FDYDYDGLHDTEDKIKEYVEGSSIPVPHYSITTSCLDETADKCDGFLPSVSSFFILPH 850
XX	Disclosure; Page -; 126pp; English.	Db	734 fdnydg1rdtedeikqyvegssipvphysitsscldtqpadkcdgplsvssffilph 793
XX	The present sequence is variant (R265K) of rat autotoxin protein.	QY	851 RPDNEESCNSSSEDESKWVEELMKMHTARYRDIEHLTSLDEFRKTSRSYPEEITLKTLYLHT 910
CC	Autotoxin is a glycoprotein cytokine which increases insulin	Db	794 rpndescsedeskwveelmkmtarvrdiehltgldfyrktsrsyeitlktylht 853
CC	signalling in adipose tissue by producing substrate for adenosine		
CC	receptors, resulting in inhibition of lipolysis, decreased hepatic		
CC	gluconeogenesis and serum glucose levels, and increased insulin		
CC	sensitivity. It also inhibits differentiation of adipocytes.		
CC	Autotoxin has type I phosphodiesterase, adenosine-5'-triphosphatase		
CC	(ATPase) and ATP pyrophosphatase activities. Autotoxin and its		
CC	analogues are used to stimulate glucose uptake by cells, particularly		
CC	to reduce serum glucose levels for treatment of non-insulin dependent		
CC	diabetes (NIDDM) in humans, or generally any condition associated		
CC	with elevated serum levels of glucose, lipid or free fatty acid		
CC	(e.g. obesity or dyslipidemia). Transgenic animals that overexpress		
CC	autotoxin are models for human metabolic diseases.		
CC	Note: The present sequence is not shown in the specification		
CC	but is derived from rat autotoxin protein sequence found in		
CC	page 101-104 of sequence listing (AY71986).		
XX	Sequence 858 AA;	SQ	911 YESEI 915
XX		Db	854 yesei 858
			RESULT 9
			AY71986
		ID	AY71986 standard; Protein; 858 AA.
		XX	AY71986;
		AC	
		XX	AY71986;
		DT	28-MAR-2001 (first entry)
		XX	
		DE	Rat autotoxin protein.
		XX	
QY	11 QIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPPWTNISGCKGRCFELQEAQ 70		
Db	7 rvislfafaisvniclgftasrikrae-wdegpptvlsdsppwtntsgckgrcfelqevg 65		
QY	71 PPDCRCNDNLCKSYTSCCCHDFDELCLKTAGWECKDRCGEVRNEENACHCSEDCLARGDC 130		
Db	66 ppdcrcdnlcncksyssccchdfdelclktargweckdrgevrneenachcsedclsrgdc 125		
QY	131 CTNYQVYCKGESSHWDCEEIKAAECAGFVRPLLIFSVDFRASYMKGSKVMNPNE 190		
Db	126 ctnyqvckgeshwvdcccceikvpecpagfvrrpliifsvdfrasymkgskvmnpie 185		
		OS	
		FH	
		Key	Location/Qualifiers

FT	Misc-difference 194 /note= "Wild type Ala substituted by Val"	Db	320	-----mtnpnreidktvqglmdg1kqqlrlhrcvnnifvgdmgmedvtcdrtfslsnylt	373
XX	WO2000068386-A1.	QY	431	NVDDITLVPGTGLRIRSKFESNNAKYDPKAIANLTCKKPQHFKPYLKQHLPKRLHYANN	490
PN	16-NOV-2000.	DB	374	: : : : : : : : : : : nvditiyptgtlgriraksinnskydkptkianltckkpqhfikpymkqhlpkrlyhann	433
XX	05-MAY-2000; 2000WO-US12402.	QY	491	RRIEDIHLVERWHARKPLDVYKKPSGKCFFGDHFDFDNKVNNSMQTVFVGYGGPTFKYK	550
PF	PR 07-MAY-1999; 99US-0306979.	DB	434	rriedihllydrwharkpldvkpkpsqkccffqgdhgfdnkvnsmqtvfvgyggptfkry	493
XX	(ZYMO) ZYMOGENETICS INC.	QY	551	TKVPPFENIELYNVMCDLLGLKPAPEENNTHGSLNHLRLRTNTFRPTMPEEVTRPNYPGIMY	610
PA	PI Kelly JD;	DB	494	tkvppfenielynvmcdllglkpaapevnmcldqkpsqncnlhrlirntfrptmpdevsrpnypgimy	553
XX	WPI; 2001-007397/01.	QY	611	LQSDFDLGCTCDDKVEPKKNKLDELNLKRLHTKGSTEERHLLYGRPAVLRYTRYDILYHTDF	670
DR	DR Disclosure; Page - ; 126pp; English.	DB	554	lqsefdlgctcdkvepkknkleelnkrlhtkgsteerhlygrpavlyrtsdilyhtdf	613
XX	New autotaxin Proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -	QY	671	ESGYSEIFMLLWTTSYTYSKQAEVSSVSPDHLTSCVRPDVRVSFSQNCLAYKNDKQMSY	730
PT	PT	DB	614	esgyseifmlplwtsytiskqaevssipehltncvrpdvrvspgsqncnlaykndkqmsy	673
XX	The present sequence is variant (A194V) of rat autotaxin protein.	QY	731	GFLFPYLSSSPEAKYDAFLVTNMPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPI	790
CC	Autotaxin is a glycoprotein cytokine which increases insulin sensitivity. It also inhibits differentiation of adipocytes.	DB	674	gflfpypylssspakydaflvtnmvpmpafkrvwayfqrvlvkkyaserngvnvvisgpi	733
CC	Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.	QY	791	FDYDYGGLHDTEDKIQYYVEGSSIPVPTHYSITTSCLDEFQPADKCDGPLSVSSFFILPH	850
CC	Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAV71986).	DB	734	fdnydgldtdeikqyvegssipvpthysitscldftqpadkcdqplsvssffilph	793
CC	CC	QY	851	RPDNEESCNSSSEDESKWVEELMKMHTARYRDIEHTLTSLDFFRKTSRSYPEBILTLKTYLHT	910
CC	CC	DB	794	rpndescnssedeskwveelmkmhtaryrdiehtlgdfyrktsrsyseiltktylht	853
CC	CC	QY	911	YESEI 915	911
CC	CC	DB	854	yesei 858	854
XX	RESULT 11				
SQ	Sequence 858 AA;	ID	AAV71995	standard; Protein; 858 AA.	
XX		XX			
Query	Match 88.18; Score 4423.5; DB 22; Length 858;	AC	AAV71995;		
Best Local Similarity 88.68; Pred. No. 0;	Mismatches 30; Indels 20; Gaps 2;	XX	28-MAR-2001 (first entry)		
Matches 802; Conservative 30; Mismatches 20; Indels 53; Gaps 2;		XX	Rat autotaxin variant (A93V).		
Db	11 QIISLETFAVGSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCKGRCFELQEAG 70	DE			
QY	7 rvisiftfaivnigftasrikrae-wdegptvlisdspwtntsgscckgrcfelqevg 65	XX	Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.		
Db	71 PPDCRCNDLNLCYSYTSCCHDDELCLKTARGWECKDRCGEVNNEAACHCSEDCLARGDC 130	KW			
QY	66 ppdcrcndlnlcysscchdfeclktargweckdrcgenvneenachcsedclsrgdc 125	KW			
Db	131 CTNYQVYCKGEHWWVDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIE 190	KW			
QY	126 ctnyqvckgehwddceeiakvpecpagfvrrpliifsvdgfrasymkkgskvmpnie 185	KW			
Db	191 KLRS CGTHPLWITATKQGVKAGTFFWVYIPHERRILTLPLDHERPSVYAFYSEQ 250	OS			
QY	186 kirscgthplwitatqgvrqgtffwsvsipherriltilqwlspdnerpssyafyseq 310	OS			
Db	246 nhrwqgqpliwlataqgvrqgtffwsvsipherriltilqwlspdnerpssyafyseq 305	OS			
QY	251 NHRWWGGQPLWITATKQGVKAGTFFWVYIPHERRILTLPLDHERPSVYAFYSEQ 245	XX			
Db	311 PDFSGHKYGPFPPEESSYGSPTPAKRPKRKVAPKRRQERPVAFFYSEQ 370	PN	W0200068386-A1.		
QY	306 pdfsghkypfpe-----	XX			
Db	319	PR	07-MAY-1999; 99US-0306979.		
QY	371 ETRQDKMTNPLREIDKIVGQLMDGLKOLKLRRRCNVNIFVGDIHGMEDVTCDRTEFLSNLT 430	PA	(ZYMO) ZYMOGENETICS INC.		
XX	XX	XX	XX	XX	

PI Kelly JD;
 XX WPI; 2001-007397/01.
 DR
 XX
 PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX Disclosure; Page - ; 126pp; English.
 XX
 CC The present sequence is variant (A93V) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic
 CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AY71986).

SQ Sequence 858 AA;

Query Match 88.1%; Score 4422.5; DB 22; Length 858;
 Best Local Similarity 88.5%; Pred. No. 0;
 Matches 801; Conservative 31; Mismatches 20; Indels 53; Gaps 2;

QY 11 QIISLFTFAVGVSICLGETAHIKRAEGWEEGPPPTVLSDPWTNISGSCKGRCFELQEAG 70
 Db 7 rvislftfaivsniclgftasrikrae-wdeggptvlsdpwtntsgsckgrcfelqevg 65
 QY 71 PPDRCRCDNLCKSYTSCTSCCHDFDELCLKTARGWECTKDRCGEVVRNEENACHCSEDCLARGDC 130
 Db 66 ppdcrcdnlicksyyssccchdfdelclktvrgwectkdrgevrneenachcsedclsrgdc 125
 QY 131 CTNYQVVKGESSHWWDDCEEIKAAECAPGFVRPPLIIFSYDGFRASYMKKGSKVMPNIE 190
 Db 126 ctnyqvvckgeshwddceelkvpccpagfvrrpliifsvdggfrasyymkkgskvmpnie 185
 QY 191 KLRSCGTHSPYMRPVYPTKTFPNLYLATGLYPESHGIVGNNSMYDPVFDATPHLGREKF 250
 Db 186 kirsctghapymrpvypptktpnlylatglypeshgivgnsmypyfdasfhlgrekf 245
 QY 251 NHRWWGGQPLWITATKQGVKAGTFFWSVVVIPHERRILIRWLTLDPHRSVYAFYSEQ 310
 Db .246 nhrwggqplwitatkqgvragtfwwsvipherrilqlwslpdnerpsvyafyseq 305
 QY 311 PDFSGHKYGPFGPEESSYGSPPFTPAKRPKRKVAPKRRQERPVAPPKKRRKTHRMDHYAA 370
 Db 306 pdfsghkqygpfgpe----- 319
 QY 371 ETRODKMTNPRLREIDKIVGQLMDGLKQLRRCVNVIYFGDHGMEDVTCDRTEFLSNLT 430
 Db 320 -----mtnplreidktvqq1mdg1kqrlhrcvnvfvgdhqmedvcdrtfesnylt 373
 QY 431 NVDITLVPGLGRIRSKFSNNAKYDPKAIIANLTCKKPDKDQHFPKYLQHLPKRLHYANN 490
 Db 374 nvdditlvpqtlgriraksinnskydpktian1tckkpdkqhfkpymkqhlprkrlhyann 433
 QY 491 RRIEDIHLVERRWHARKPLDVYKPKPSGKCFQGDHNKVNNSMQTVFVGYPGPTFKYK 550
 Db 434 rriedihl1vdrrwharkpldvykpksgkcfqgdhgfdnkvnsmqtvfvgypgtfkry 493
 QY 551 TKVPPFENIELYNVMCDLGLKPKAPNNNGTHGSINHLLRTNTFRPTMPEEVTRPNYPGIMY 610
 Db 494 tkvppfenielynvmcdlglkpkapnnthgslnhllrtntfrptmpevsrpnypgimy 553

QY 611 LQSDFDLGCTCDDKVEPKNKLDDELNRKLHHTKGSTEERHLLYGRPAVLRTTRYDILYHTDF 670
 Db 554 1qsefd1gctcddkvepknkkleelnkrhltkgsteerhlygrpavlyrtsydlyhtdf 613
 QY 671 ESGYESEIFMLLWNTSYTVSKQAEVSSVSPDHLSCSVRPDVRSPSFSQNCLAYKNDKQMSY 730
 Db 614 esgyeiflmplwtsytiskqaevssipehltncrvrpsqfsqnclaykndkqmsy 673
 QY 731 GFLFPYISSLSSPEAKYDAFLVYTNMVPMYPAFKRVWNYFQRVLYVKYASERNGVNVISGPI 790
 Db 674 gflfppylsspeakydaflvtnmvpmpafkrywayfqrvlvkyaserngvnvisgpi 733
 QY 791 FDYDXDGLADTEDKIKQYVSEGSSIPVPTHYSITSCLDFTQPADKCDGPLSVSSPFILPH 850
 Db 734 fdnydg1rltdeikqyvegssipvpthysitscldtfqpadkcdgplsvssfilph 793
 QY 851 RPDNEESCNSSDESEKSWEEILMKMHTARVRDIEHLTSLSDFEFFRKTSRSYPEILTLKTYLHT 910
 Db 794 rpndescnssedeskwveelmkmhtarvrdiehltgldfyrtksrsyseiltlktylht 853
 QY 911 YESEI 915
 Db 854 yesei 858
 RESULT 1.2
 AAR86595
 ID AAR86595 standard; Protein: 849 AA.
 XX
 XX
 AC AAR86595;
 DT 01-JUL-1996 (first entry)
 XX
 DE N-tera 2D1 autotoxin protein.
 XX
 KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
 XX melanoma cell; tumour; antibody; cancer diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9532221-A2.
 XX
 PD 30-NOV-1995.
 XX
 PF 24-MAY-1995; 95WO-US06613.
 XX
 PR 28-NOV-1994; 94US-0346455.
 PR 25-MAY-1994; 94US-0249182.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M,
 XX
 PR WPI; 1996-020533/02.
 XX
 PT Autotaxin motility stimulating protein, and DNA encoding it - used
 PT in cancer diagnosis and therapy
 XX
 PS Claim 4; Page 86-89; 112pp; English.

CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
 CC sequence represents the full length protein sequence of the
 CC teratocarcinoma N-tera 2D1 ATX protein. ATX is an autocrine motility
 CC stimulating protein which is present in cancer cells. ATX stimulates
 CC both random and directed migration of melanoma cells. The tumourous
 CC form of ATX is a secreted protein, while the transmembrane bound form is
 CC not present in tumour cells. The cDNA encoding this sequence can be used
 CC in a vector, to transform cells. The recombinant cells can then be used
 CC to produce the peptide sequences. Antibodies specific for these
 CC sequences can be produced, and can be used in cancer diagnosis and
 CC therapy. Different sites of localisation of the protein are utilised for
 CC diagnosis and prognosis of the stages of tumour progression. The

CC sequences can be used in treatment methods to advantageously block the
CC activity of the secreted form of AXT, while having little effect on the
CC membrane form of AXT.

XX Sequence 849 AA;

SQ Query Match 86.5%; Score 4341; DB 17; Length 849;

Best Local Similarity 87.9%; Pred. No. 0;

Matches 811; Conservative 11; Mismatches 19; Indels 82; Gaps 7;

XX

RESULT 13

ARY71989

ID AAY71989 standard; Protein; 885 AA.

XX

AC AAY71989;

XX

DT 28-MAR-2001 (first entry)

XX

Rat brain autotoxin designated as PD-Ialpha.

XX

DE

Db 827 ktsrsypeeilktlytseyei 849

CC membrane form of AXT.

XX

CC

Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF; melanoma cell; tumour; antibody; cancer diagnosis; therapy.						
Db	1	marqgcldsfqvvislftfaaisvniciqftasrikrae-wdegpptvlsdpswtnsgsck	59	KW	Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;	
QY	61	GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKXTARGWECTKDRCGEVNRNEENACHC	120	KW		
Db	60	grcfelqevgppdcrcdnlkcsccchdfdelclktvrgwectkdrsgevrneenachc	119	XX		
				OS	Homo sapiens.	
				XX		
				PH	Location/Qualifiers	
QY	121	SEDCLARGDCCTNQVVKGESHWDD-----DCEEEIKAAECPAGFVRPPLIIFSVVDG	173	FT	Key MISC-difference 864 /note= "unspecified amino acid"	
Db	120	pedclsrgdcctnyqvvcckgeshwddaaarnqssec1qv----cp----ppliifsvdg	170	FT	Misc-difference 889 /note= "unspecified amino acid"	
QY	174	FRASYMKKGSKVMPNIEKLRSCTGHSPYMPMRPVYPTKTFPNLYLTATGLYPESHGIVGNSM	233	FT	Misc-difference 905 /note= "unspecified amino acid"	
Db	171	frasymkkgskvmpniek1rsctghpyptrpyptktpnlyltatglhypeshgivgnsm	230	FT	Misc-difference 911 /note= "unspecified amino acid"	
QY	234	YDPVFEDATFHLLRGREKEFKHNRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTLRWL	293	FT	Misc-difference 927 /note= "unspecified amino acid"	
Db	231	ydpvf dasfhlrgrekfnhrwwggqlwitatkqgvragtffwsvsipherril1qwl	290	FT	Misc-difference 937 /note= "unspecified amino acid"	
QY	294	TLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPTTPAKRPKRQERPVVA	353	FT	Misc-difference 944 /note= "unspecified amino acid"	
Db	291	s1pdnerpsvyaafyseqpdfsgkhgpfge-----	321	FT	Misc-difference 950 /note= "unspecified amino acid"	
QY	354	PKKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIIFVGDHG	413	FT	Misc-difference 954 /note= "unspecified amino acid"	
Db	322	mtnp1reidktvgq1mdglkq1rlhrcvnvifvgdhg	358	FT	Misc-difference 967 /note= "unspecified amino acid"	
QY	414	MEDVTCDRTEFLSNYLTVNDDITLVPGTLGRIRSKEFSNNAKYDPKAIIANLTCKKPQDHF	473	FT	Misc-difference 975 /note= "unspecified amino acid"	
Db	359	medvtcdrteflsnyltnvdditlvpgtlgriraksinnskydpktianltckkpqdhf	418	XX		
QY	474	KPYLKQHLPKRLHYANNRRIEDIHILLVERRWHVARKPLDVYKKPSGKCFQGDHGFDNKV	533	PN	WO9532221-A2.	
Db	419	kpymkqhipkrlhyanrriedihllvdrwhvarkpldvkpsgkcfqgdhgfdnkv	478	XX	30 - NOV - 1995.	
QY	534	NSMQTIVFVGYGPTFYKTKVPPFENIELYNMCDLLGLKPAPNGNTGSLNHILLRTNTFR	593	PD	PD	
Db	479	nsmqtvfvgygptfykrtkvppfenielynvmcdll91kpa pingthgslnhillrtntfr	538	XX	24 - MAY - 1995;	95WO-US06613.
QY	594	PTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDENKLHTKGSTE-----	645	XX	PR	
Db	539	ptmpdevsrpnypgimylqsefdlgctcdkvepknkleelnkrhlgfslhllrtntfr	538	XX	PR	28 - NOV - 1994;
QY	646	599 skhenkknngsveprkerhlygrpavlyrtsydlyhtdfesgyseif1mplwtstyti	658	XX	PR	25 - MAY - 1994;
Db	599	skqaevssipehltncvrpdvrvspgfqsnclayknokqmsyqflfppyysspeakyda	718	XX	XX (USSH) US DEPT HEALTH & HUMAN SERVICES.	
QY	689	SKQAEVSSVPDHILTSCVRPDVRSFSQNCLAYKNDKOMSYGFLEPPYLSSEAKYDA	748	PA	Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;	
Db	659	skqaevssipehltncvrpdvrvspgfqsnclayknokqmsyqflfppyysspeakyda	718	XX	WPI; 1996-020533/02.	
QY	749	FLVTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPIFDYDGLHDTEDKIKY	808	XX	Autotaxin motility stimulating protein, and DNA encoding it - used in cancer diagnosis and therapy	
Db	719	flvtnmvpmypafkrvwayfqrvlvkkyaserngvnvisgpfdynqdglrdtedikqy	778	XX	Claim 4; Page 67-70; 112pp; English.	
QY	809	VEGSSIPVPTHYYSIITSCLDFTOPADKCDGPLSVSSFILPHRDNEECSNSSEDESKWV	868	CC	AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourous form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of ATX, while having little effect on the membrane form of ATX.	
Db	779	vegssipvpthyysiiitscldfqpadkcdgplsvssfilphrdndesnsedeskwv	838	CC	Sequence 979 AA;	
QY	869	EELMKMHTARVTDIEHTLSDLFFRKTTSRSPYPEILTLKTYLHTYESEI	915	CC	Query Match 85.3%; Score 4279; DB 17; Length 979;	
Db	839	eelmkmhtarvrdiehtlgldfyrktsrsyseiltkty1htyesei	885	CC	Best Local Similarity 87.1%; Pred. No. 0; Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps DT	
				RESULT 14		
				AAR86580 standard; Protein; 979 AA.		
				AAR86580; AC 28-JUN-1996 (first entry)		
				Autotaxin derived from human liver cells.		
				1 MARRSSFOSCOIIISLFTFAVGVSICLGFATAHKRAEGWEEGPPTVLSDSPWTNISGSCK 60 DE		

Db	1	marrssfqscqdislftfavgvniclgftahrikraegweegpptvlisdspwtnisgsck	60	KW	Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
QY	61	GRCFELQEAGPPDCRCDNICKSYTSSCCHDDELCLKTARGWECTKDRCGEVNEENACHC	120	KW	melanoma cell; tumour; antibody; cancer diagnosis; therapy.
Db	61	grcfelqeagppdcrcdnlicksytscchdffdelclktarawectkdrgevrneenachc	120	XX	
QY	121	SEDCLARGDCTNYQVVKGESHWVDDCEEIKAAECPAGFVRPPLIIFSVWDGF--RASY	178	OS	Homo sapiens.
Db	121	sedclargdctnyqvvckgeshwvddceiakaeciq--vcspsinhlrgwlpmnts	178	XX	
QY	179	MKKGSKXVMPNIEKLRSCTHSPYMPVYPTKTFPNLYTLATGLYPESHGIVGNNSMYDPVF	238	XX	
QY	179	mkkgskxvmpnieklrscthspymrvpyptkfpnlytlatglpeshgivgnsmypv	238	XX	
QY	239	DATFHLRGREKFNRWWGGQPLWITATKQGVKAGTFFWSVV-----PHERRILTILRWLT	294	XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
Db	239	datfhlrgrrekfnhrwggqplwitatkqrges----wnillvcchpsraeiltlqlwt	294	XX	
QY	295	LPDHERPSVYAFYSEQPDESGHKYGPFGPEESSYGSPTPAKRPKRKVAPKRQERPVAP	354	XX	
Db	295	lpdherpsvafyseqpdfsgkhmpfge-----	324	XX	Autotaxin motility stimulating protein, and DNA encoding it - used
QY	355	PKKRRRKIHRMDHYAAETRQDKMTNPRLREIDKIVGQLMDGLKQLKLRRCVNVIIFVGDHGM	414	XX	PT in cancer diagnosis and therapy
Db	325	-----mtnp1remhkivgqlmdglkq1k1hrcvnvifv---et	359	PS	Claim 4; Page 62-65; 112pp; English.
QY	415	EDVTCD--RTEFLSNVYDDITLWPGTLGRIRSKFSNNNAKYDPKAIIANLTCKKPQDH	472	XX	AAR86559-R865596 represent autotaxin (ATX) and fragments of it. ATX is
Db	360	mdgrchmyrteflsnlytndditlvgptlgrirskfsnnakydpkaianltckkpqdh	419	CC	an autocrine motility stimulating protein which is present in cancer
QY	473	EKPYLKQHLPKRLHYANNRRIEDIHLLVERRVHVARPKLDVYKKPSGKCFEQGDHGFDNK	532	CC	cells. ATX stimulates both random and directed migration of melanoma
Db	420	fkyplkqhipkrlhyannriedihllverrvhvarpkldvyykkpsgnafsrrettafdnk	479	CC	cells. The tumourous form of ATX is a secreted protein, while the
QY	533	VNSMQTYFVGYGPTEKYKTKVPPFENIELYNYMCDLIGLKAPAPNGTHGSINHLLRTNTF	592	CC	transmembrane bound form is not present in tumour cells. The cDNA
Db	480	vnsmqtvfygqptfkkytkvppfenielynvmcdllgkppapngthgsinhlrrntf	539	CC	encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used to produce the peptide sequences.
QY	593	RPTMPEEVTRPNYPGIMYLQSDFEDLGCTCDDKVEPKNKLDLNKRLHTKGSTEERHLLYG	652	CC	Antibodies specific for these sequences can be produced, and can be used
Db	540	rptmpeevtrpnypgimylqsdffd1gctcdkvepknkldelnkrh1lyg	599	CC	to localisation of the peptide sequences. Different sites of localisation of the peptide sequences can be used in diagnosis and prognosis of the stages of tumour
QY	653	-RPAVLYTRYDILYHTDFESGYSEIFMLLIWTSYTYSKQAEVSSVPDHLTSCVRPDVRV	711	XX	having little effect on the membrane form of ATX, while
Db	600	drpavlytrydilyhdtdfesgyseifmlplwtsytvsqaevssvpdhltscvrpdrv	659	XX	having little effect on the membrane form of ATX, while
QY	712	SPSFSONCLAYKNDKQMSYGFLLPPLSSSPEAKYDAFLVLTNMVPMYPAFKRVWNHYFQRV	771	XX	having little effect on the membrane form of ATX, while
Db	660	spsfsqnclaykndkqmsygfllfppylsspeakydaflvtnmvpmpyafkrvwnhyfqr	719	XX	having little effect on the membrane form of ATX, while
QY	772	LVKKYASERNGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSISITSCLDFT	831	XX	having little effect on the membrane form of ATX, while
Db	720	lvkkyaserngvnvisgpi.fdydydglhdtedkikqyvegssipvptphyysisitscldf	779	XX	having little effect on the membrane form of ATX, while
QY	832	QPADKCDDGPLSVSSFILPHRPDNEESCNSSEDESKEELMRMHTARYRDIEHLTSLDF	891	XX	having little effect on the membrane form of ATX, while
Db	780	qpadkdgp1svssfilphrpdeeescnssedeskwveelmkmhtaryrdiehltsldff	839	XX	having little effect on the membrane form of ATX, while
QY	892	RKTTSRYPEIILTLKTYLHTYESEI	915	XX	having little effect on the membrane form of ATX, while
Db	840	rkttsrypeiitlktylhtyesei	863	XX	having little effect on the membrane form of ATX, while
QY	310	QPDSFGHKYGPFGPEESSYGSPTPAKPKRKVAPKRRQERPVAPPKKRMRDHYA	369	XX	
Db	235	qpdfsghkhpfgpe-----	-----	XX	
QY	370	ATRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIIFVGDHGMEDVTC-----RTEFLSN	427	XX	
Db	250	-----mnpnplremhkvq1mdq1kq1khrvnnifv---etmdgrchmyrteflsn	299	XX	
QY	428	YLTNVDDITLVPGTGLRIRSKFSNNAKYDPKAIANLTCKPQDQHFKPYLQHLPKRLHY	487	XX	Autotaxin derived from teratocarcinoma N-tera 2D1 cells.

Db	300	Yltvvdditlvpgt.lgrirrskfsnnakydpkaianltckkpdqhfkpypylkqhlpkrly	359
Qy	488	ANNRRIEIHLLVERRWHVARKPLDVKKPSGKCFQGDHGFDNKVNISMOTVFGYGYPTF	547
Db	360	annriedihlverrwvarpldvykkpsgnafsrrettafdnkvnsmqtvfgygptf	419
Qy	548	KYKTKVPPFENIELYNVMCDLGLKAPANNNGTHGSLNHLRNTFRPMPEEVTRPNPG	607
Db	420	kyktkvppfenielynvmcdllgkappngthfslnhlrlntfrpmpeevtrpnpg	479
Qy	608	IMYLQSDFDLGLCTCDDKVEPKNLDELNKRRLHTKGSTEERHLLYG-RPAVLYRTRYDILY	666
Db	480	imylqsdfdlglctcdkrepknkldeelnkrllhtkgsteerhllgdrpavlyrttrydil	539
Qy	667	HTDFEESGYSEIFMLLIWTSYTWSKQAEVSSVPDHLTSCVRPDVRSFSFSQNCLAYKNDK	726
Db	540	htdfesgyseifmlplwtsytvkqaevssvpdhltscvrpdvrspsfsqnclaykndk	599
Qy	727	QMSYGFIFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVNNYFORVLWKKYASERNGVNNV	786
Db	600	qmsygg1gppylsspeakydaflvttnmvpmpafkrvnnyfqrvlvkyaserngvnnv	659
Qy	787	SGPIDFYDGLHDTEDKIKQYVEGSSIPVPTHYSSILITSCLDFTOPADKCDGPLSVSSF	846
Db	660	sgpifdydglhdtedkikqyvegssipvptyssilitscldftopadkcdgplsvssf	719
Qy	847	ILPHRPDNEESCNSSEDBKWEELMKMHTARVRDIEHLLTSLDFFRKTSRSYPEILTLKT	906
Db	720	ilphrpdneescnssedeskwveelkmhtarvrdiehltstdffrktsrsypeiltlkt	779
Qy	907	YLHTYESEI 915	
Db	780	ylhtyesei 788	

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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:42:27 ; Search time 20.45 Seconds
 (without alignments)
 901.337 Million cell updates/sec

Title: US-09-483-831-69
 Perfect score: 5019
 Sequence: 1 MARRSSEQSCQITISLTFEA... RSYPEILTKYLHTYESEI 915

Scoring table: BLOSUM62
 Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters : 193259

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:
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 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
 .5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	5019	100.0	915	1	US-08-346-455B-69	Sequence 69, Appl
2	5019	100.0	915	3	US-08-977-221-69	Sequence 69, Appl
3	5019	100.0	915	5	PCT-US95-06613-69	Sequence 69, Appl
4	4533	90.3	829	1	US-08-346-455B-34	Sequence 34, Appl
5	4533	90.3	829	3	US-08-977-221-34	Sequence 34, Appl
6	4533	90.3	829	5	PCT-US95-06613-34	Sequence 34, Appl
7	4418	88.0	861	1	US-08-346-455B-67	Sequence 67, Appl
8	4418	88.0	861	3	US-08-977-221-67	Sequence 67, Appl
9	4418	88.0	861	5	PCT-US95-06613-67	Sequence 67, Appl
10	4279	85.3	979	1	US-08-346-455B-38	Sequence 38, Appl
11	4279	85.3	979	3	US-08-977-221-38	Sequence 38, Appl
12	4279	85.3	979	5	PCT-US95-06613-38	Sequence 38, Appl
13	3842	76.5	788	1	US-08-346-455B-36	Sequence 36, Appl
14	3842	76.5	788	3	US-08-977-221-36	Sequence 36, Appl
15	3842	76.5	788	5	PCT-US95-06613-36	Sequence 36, Appl
16	1955.5	39.0	873	3	US-09-187-331-6	Sequence 6, Appl
17	1955.5	39.0	925	2	US-08-392-946-1	Sequence 1, Appl
18	1955.5	39.0	925	2	US-08-504-169-1	Sequence 1, Appl
19	1955.5	39.0	925	5	PCT-US94-14893-1	Sequence 1, Appl
20	360	7.2	438	3	US-09-187-331-2	Sequence 2, Appl
21	357	7.1	355	2	US-09-014-969-19	Sequence 19, Appl
22	192	3.8	39	1	US-08-346-455B-54	Sequence 54, Appl
23	192	3.8	39	3	US-08-977-221-54	Sequence 54, Appl
24	192	3.8	39	5	PCT-US95-06613-54	Sequence 4, Appl
25	126.5	2.5	2471	4	US-09-112-450-4	Sequence 84, Appl
26	123	2.5	4654	4	US-08-476-515A-84	Sequence 84, Appl
27	123	2.5	4655	4	US-08-652-877-84	Sequence 84, Appl

Print good job

RESULT 1
 US-08-346-455B-69
 ; Sequence 69, Application US/08346455B
 ; Patent No. 5731167
 /GENERAL INFORMATION:
 /APPLICANT: UNITED STATES OF AMERICA; DEPT.
 /APPLICANT: OF HEALTH AND HUMAN SERVICES
 /TITLE OF INVENTION: MOTILITY STIMULATING
 /TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 /TITLE OF INVENTION: THERAPY
 /NUMBER OF SEQUENCES: 69
 /CORRESPONDENCE ADDRESS:
 /ADDRESSEE: MORGAN & FINNEGAN
 /STREET: 345 PARK AVENUE
 /CITY: NEW YORK
 /STATE: NEW YORK
 /COUNTRY: U.S.A.
 /ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 17-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 202-6-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 69:
 LENGTH: 915
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: cDNA
 MOLECULE TYPE: cDNA

; HYPOTHETICAL: No
; FEATURE: NAME/KEY: A2058 ATX protein
; LOCATION: IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-346-455B-69

Query Match 100.0%; Score 5019; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWECPPTVLSDSPWNTNISGSCK 60
Db 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWECPPTVLSDSPWNTNISGSCK 60

QY 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNNEENACHC 120
Db 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNNEENACHC 120

QY 121 SEDCLARGDCCTNYQVVCKGE SHWVDDCEEEKAEC PAGFVRPPLIIFSVDFRAS YMK 180
Db 121 SEDCLARGDCCTNYQVVCKGE SHWVDDCEEEKAEC PAGFVRPPLIIFSVDFRAS YMK 180

QY 181 KGSKYMPNIEKLRS CGTHSPYMRPVYPTKTFPNLYTLATGLYPE SHGTYGNSM YDPVFDA 240
Db 181 KGSKYMPNIEKLRS CGTHSPYMRPVYPTKTFPNLYTLATGLYPE SHGTYGNSM YDPVFDA 240

QY 241 TEHLRGREKF NH RWWGGQLWITATK QGVKAGTF FWSVVPIPHERRITLIRWLTLPDHER 300
Db 241 TEHLRGREKF NH RWWGGQLWITATK QGVKAGTF FWSVVPIPHERRITLIRWLTLPDHER 300

QY 301 PSVYAFYSEQPDPFGSHKYGPFGPEESSYGS PFTPAKRPKRKVAPKRQERPVAPPKRRR 360
Db 301 PSVYAFYSEQPDPFGSHKYGPFGPEESSYGS PFTPAKRPKRKVAPKRQERPVAPPKRRR 360

QY 361 KIHRMDHYAAE TRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVI FVG D HGM EDV TCD 420
Db 361 KIHRMDHYAAE TRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVI FVG D HGM EDV TCD 420

QY 421 RTEFLSNYLTVDDITLVPGTLGRIRS KFSNNAKYDPKAIIANLTICKPDKDQHFKPYLKQH 480
Db 421 RTEFLSNYLTVDDITLVPGTLGRIRS KFSNNAKYDPKAIIANLTICKPDKDQHFKPYLKQH 480

QY 481 LPKRLHYANNR RIEDIHL LVER RW H VARKPLD WYKKPSGK CFF QGDHFDNKVN SMQTVF 540
Db 481 LPKRLHYANNR RIEDIHL LVER RW H VARKPLD WYKKPSGK CFF QGDHFDNKVN SMQTVF 540

QY 541 VGYGPTFKYKTKVPPFEN IELVN MCDL GLKFA P NNGTHGS LNL LRTNTFRPTMPEEV 600
Db 541 VGYGPTFKYKTKVPPFEN IELVN MCDL GLKFA P NNGTHGS LNL LRTNTFRPTMPEEV 600

QY 601 TRPNYPGIMYLQSDFDLGCT CDDKVEPKNKLDELNKLRLHTKGSTEERHLLYGRPAVLYRT 660
Db 601 TRPNYPGIMYLQSDFDLGCT CDDKVEPKNKLDELNKLRLHTKGSTEERHLLYGRPAVLYRT 660

QY 661 RDILYHTDFESGYSEI FMLI WTTSVSKOAEVSSVPDH LTSCVRP DVSPFSQNCL 720
Db 661 RDILYHTDFESGYSEI FMLI WTTSVSKOAEVSSVPDH LTSCVRP DVSPFSQNCL 720

QY 721 AYKNDKQMSYGF LFPPYLS SPEAKYDAFLV TNMVPM PMAFKRVWN YFQRVLVKKYASER 780
Db 721 AYKNDKQMSYGF LFPPYLS SPEAKYDAFLV TNMVPM PMAFKRVWN YFQRVLVKKYASER 780

QY 781 NGVNVISGP IFDYDGLHDTEDKIKYVEGSSIPVPTHYSIITSCLDFTQPADKCDGP 840
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QY 841 LSVSSFILPHRDNEECS SSEDSESKWVEELMKMHTARV DIEH L TSDFRKT SRV PTE 900
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RESULT 2
US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149U3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-977-221-69

Query Match 100.0%; Score 5019; DB 3; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSSFOSCOQIISLFTFAVGVSICLGFTAHRIKRAEGWECPPTVLSDSPWNTNISGSCK 60
Db 1 MARRSSFOSCOQIISLFTFAVGVSICLGFTAHRIKRAEGWECPPTVLSDSPWNTNISGSCK 60

QY 61 MARRSSFOSCOQIISLFTFAVGVSICLGFTAHRIKRAEGWECPPTVLSDSPWNTNISGSCK 60
Db 1 MARRSSFOSCOQIISLFTFAVGVSICLGFTAHRIKRAEGWECPPTVLSDSPWNTNISGSCK 60

QY 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNNEENACHC 120

STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 915
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: No
 FEATURE:
 NAME/KEY: A2058 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PCT-US95-06613-69

Query Match 100.0%; Score 5019; DB 5; Length 915;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 915; Conservative 0; Missmatches 0; Indels 0; Gaps 0

QY 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60
 Db 1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60

QY 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENACHC 120
 Db 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENACHC 120

QY 121 SEDCLARGDCCTNYQVCKGESSHWDCCDEEIKAAECPAGEFVRPPLIIFSVDFRASYMK 180
 Db 121 SEDCLARGDCCTNYQVCKGESSHWDCCDEEIKAAECPAGEFVRPPLIIFSVDFRASYMK 180

QY 181 KGSKVMPIEKLRSGGTHSPYMRPVYPTKTFPNLYTTLATGLYPSHGIVGNSMYDPVFDA 240
 Db 181 KGSKVMPIEKLRSGGTHSPYMRPVYPTKTFPNLYTTLATGLYPSHGIVGNSMYDPVFDA 240

QY 241 TPHLRGREKEFHRTWGGPQLWITATKGVKAGTFWSVVIPHERRILTLRWLTLPDHER 300
 Db 241 TPHLRGREKEFHRTWGGPQLWITATKGVKAGTFWSVVIPHERRILTLRWLTLPDHER 300

QY 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPETPAKRPKRKVAPRKQRQERPVAPPKKRRR 360
 Db 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPETPAKRPKRKVAPRKQRQERPVAPPKKRRR 360

QY 361 KIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQKLRRCVNVIFVGDHGMEDVTC 420
 Db 361 KIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQKLRRCVNVIFVGDHGMEDVTC 420

QY 421 RTEFLSNYLTNVDITLVPGTGLGRIRSKFSNNAKYDPKAIIANLTCKKPQDFKPYLKQH 480
 Db 421 RTEFLSNYLTNVDITLVPGTGLGRIRSKFSNNAKYDPKAIIANLTCKKPQDFKPYLKQH 480

QY 481 LPKRLHYANNRRIEDIHLVERRWHVARKPLDVYKKPSGKCFQQGDHGFDPDNKVNNSMQTFV 540
 Db 481 LPKRLHYANNRRIEDIHLVERRWHVARKPLDVYKKPSGKCFQQGDHGFDPDNKVNNSMQTFV 540

QY 541 VGYGPTFKYKTKVPPFENIELYNVMCDDLGCTCDDKVEPKNKLDELNKRLHTKGSTERNLLYGRPAVLVRT 600
 Db 541 VGYGPTFKYKTKVPPFENIELYNVMCDDLGCTCDDKVEPKNKLDELNKRLHTKGSTERNLLYGRPAVLVRT 600

QY 601 TRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTERNLLYGRPAVLVRT 660
 Db 601 TRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTERNLLYGRPAVLVRT 660

QY 661 RYDILYHTDFESGYSEIFMLLWTSYTVSKQAEVSSVPDVRVSPFSQNCL 720
 Db 661 RYDILYHTDFESGYSEIFMLLWTSYTVSKQAEVSSVPDHLTSCVRPDSFSQNCL 720

QY 721 AYKNDKQMSYGFLEPPYLYSPEAKYDAFLVNMVPVMYPAFKRVWNYFQRVLVKKYASER 780
 Db 721 AYKNDKQMSYGFLEPPYLYSPEAKYDAFLVNMVPVMYPAFKRVWNYFQRVLVKKYASER 780

QY 781 NGVNVISGPIFYDYYDGLHDTEDKIKQQYVEGSSIPVPTHYSITSCLDFTQPADKCDGP 840
 Db 781 NGVNVISGPIFYDYYDGLHDTEDKIKQQYVEGSSIPVPTHYSITSCLDFTQPADKCDGP 840

QY 841 LSVSSFILPHRDNEECSNSEDSESKWVEELMKMHTARVARDIEHLTSLLDFRKTSRYPE 900
 Db 841 LSVSSFILPHRDNEECSNSEDSESKWVEELMKMHTARVARDIEHLTSLLDFRKTSRYPE 900

QY 901 IITLTKTYLHTYESEI 915
 Db 901 IITLTKTYLHTYESEI 915

QY 121 SEDCLARGDCCTNYQVCKGESSHWDCCDEEIKAAECPAGEFVRPPLIIFSVDFRASYMK 180
 Db 121 SEDCLARGDCCTNYQVCKGESSHWDCCDEEIKAAECPAGEFVRPPLIIFSVDFRASYMK 180

QY 181 KGSKVMPIEKLRSGGTHSPYMRPVYPTKTFPNLYTTLATGLYPSHGIVGNSMYDPVFDA 240
 Db 181 KGSKVMPIEKLRSGGTHSPYMRPVYPTKTFPNLYTTLATGLYPSHGIVGNSMYDPVFDA 240

QY 241 TPHLRGREKEFHRTWGGPQLWITATKGVKAGTFWSVVIPHERRILTLRWLTLPDHER 300
 Db 241 TPHLRGREKEFHRTWGGPQLWITATKGVKAGTFWSVVIPHERRILTLRWLTLPDHER 300

QY 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPETPAKRPKRKVAPRKQRQERPVAPPKKRRR 360
 Db 301 PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPETPAKRPKRKVAPRKQRQERPVAPPKKRRR 360

NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS: MURATA, JUN
 APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
 APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
 APPLICANT: HENRY; MURATA, JUN
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 TITLE OF INVENTION: THERAPY

Db 421 ARKPLDYYKKPSGKCKFFQGDHGFDNKVNNSMOTVFVGYGPTFKYKTKVPPFENIELYNVMC 480
 QY 567 DLLGLKPAPNINGTHGSNLNLLRTNTFRPTMPEVTRPNYPGIMYLQSDFDLGCTCDDKVE 626
 Db 481 DLLGLKPAPNINGTHGSNLNLLRTNTFRPTMPEVTRPNYPGIMYLQSDDLGCTCDDKVE 540
 QY 627 PKNKLDLNRKLHTKGSTEERHLLYGRPAVLRTTRYDILYHTDFESGYSEIFMLLWTSY 686
 Db 541 PKNKLDLNRKLHTKGSTEERHLLYGRPAVLRTTRYDILYHTDFESGYSEIFMLLWTSY 600
 ; STRAIN: INDIVIDUAL ISOLATE:
 ; DEVELOPMENTAL STAGE:
 ; HAPLOTYPE:
 ; TISSUE TYPE:
 ; CELL TYPE: Melanoma
 ; CELL LINE: A2058
 ; ORGANELLE:
 ; FEATURE:
 ; NAME/KEY:
 ; LOCATION:
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION: Putative protein
 ; OTHER INFORMATION: sequence of A2058 Autotaxin
 ; US-08-977-221-34

Query Match 90.3%; Score 4533; DB 3; Length 829;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 CHDFDELCLKTARGWECKDRGEVRENEENACHCSEDCLRGDCCTNYQVVKGESHWVD 146
 Db 1 CHDFDELCLKTARGWECKDRGEVRENEENACHCSEDCLRGDCCTNYQVVKGESHWVD 60
 QY 147 DDCEIKAECAPGFVRPPLIFSVDFRASYMKGSKVMPIEKLRSCGTHSPYMRPVY 206
 Db 61 DDCEIKAECAPGFVRPPLIFSVDFRASYMKGSKVMPIEKLRSCGTHSPYMRPVY 120
 QY 207 PTKTFPNNLYTATGLYPESHGIVGNSMYDPVFDATFLRGREKFNRWGGQPLWITATK 266
 Db 121 PTKTFPNNLYTATGLYPESHGIVGNSMYDPVFDATFLRGREKFNRWGGQPLWITATK 180
 QY 267 QGVKAGTFFWSVVIPHERRILTLRWLTPDHERPSSYAFYSEQPDFSGHKYGPFGPEES 326
 Db 181 QGVKAGTFFWSVVIPHERRILTLRWLTPDHERPSSYAFYSEQPDFSGHKYGPFGPEES 240
 QY 327 SYGSPFTPAKRPKRKVAPKRQERPVAPPKRRKIKHRMDHYAAETRODKMTNPRLREIDK 386
 Db 241 SYGSPFTPAKRPKRKVAPKRQERPVAPPKRRKIKHRMDHYAAETRODKMTNPRLREIDK 300
 QY 387 IVGQLMDGLKQLLRRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTVPGTLGRIR 446
 Db 301 IVGQLMDGLKQLLRRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTVPGTLGRIR 360
 QY 447 SKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLVERRWHV 506
 Db 361 SKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLVERRWHV 420
 QY 507 ARKPLDYYKKPSGKCKFFQGDHGFDNKVNNSMOTVFVGYGPTFKYKTKVPPFENIELYNVMC 566
 Db 421 ARKPLDYYKKPSGKCKFFQGDHGFDNKVNNSMOTVFVGYGPTFKYKTKVPPFENIELYNVMC 480
 QY 567 DLLGLKPAPNNGTGHGSNLNLLRTNTFRPTMPEEVTLPYQGIMYLQSDFDLGCTCDDKVE 626
 Db 481 DLLGLKPAPNNGTGHGSNLNLLRTNTFRPTMPEEVTLPYQGIMYLQSDDLGCTCDDKVE 540
 QY 627 PKNKDELNRKLHTKGSTEERHLLYGRPAVLRTTRYDILYHTDFESGYSEIFMLLWTSY 686
 Db 541 PKNKDELNRKLHTKGSTEERHLLYGRPAVLRTTRYDILYHTDFESGYSEIFMLLWTSY 600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 829

QY 687 TVSKQAEVSSVPDHLTSCVRPDRVSFSQNCLAYKNDKQMSYGFLLPPYLSPEAKY 746
 Db 601 TVSKQAEVSSVPDHLTSCVRPDRVSFSQNCLAYKNDKQMSYGFLLPPYLSPEAKY 660

QY 747 DAFLVTNMVPMYPAFKRVWNMFQRLVKKYASERNGVNVISGPIFDYDGLHDTEDKIK 806
 Db 661 DAFLVTNMVPMYPAFKRVWNMFQRLVKKYASERNGVNVISGPIFDYDGLHDTEDKIK 720
 QY 807 QYVEGSSIPVPTHYSSITSCLDFTQPADKCDGPLSVSSEFLPHRPDNEECSNSEDESK 866
 Db 721 QYVEGSSIPVPTHYSSITSCLDFTQPADKCDGPLSVSSEFLPHRPDNEECSNSEDESK 780
 QY 867 WVEELMKMHTARVRDIEHLLSLDFFRKTSRSYPEILTLKTYLHTYESEI 915
 Db 781 WVEELMKMHTARVRDIEHLLSLDFFRKTSRSYPEILTLKTYLHTYESEI 829
 RESULT 5
 US-08-977-221-34
 ; Sequence 34, Application US/08977221
 ; Patent No. 6084069
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT .
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MORTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/977, 221
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/346, 455
 ; FILING DATE: 28-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249, 182
 ; FILING DATE: 25-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/822, 043
 ; FILING DATE: 17-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DOROTHY R. AUTH
 ; REGISTRATION NUMBER: 36, 434
 ; REFERENCE/DOCKET NUMBER: 2026-4149US3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 829

FEATURE: ;
 NAME/KEY: ;
 LOCATION: ;
 IDENTIFICATION METHOD: ;
 OTHER INFORMATION: Putative protein
 OTHER INFORMATION: sequence of A2058 Autotoxin
 PCT-US95-06613-34

	Query	Match	Score	DB	Length
RESULT	6	90.3%	4533	5	829
PCT-US95-06613-34	QY	Best Local Similarity	99.9%	Pred. No.	0;
Sequence 34, Application PC/TUS9506613	Db	Matches	828;	Mismatches	1;
GENERAL INFORMATION:		Indels	0;	Gaps	0;
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;	QY	CHDFFDELCLKTARGWECTKDRGDEVNNEENACHCSEDCLARGDCCTNYQVVCKGEHWVD	146		
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,	Db	CHDFFDELCLKTARGWECTKDRGDEVNNEENACHCSEDCLARGDCCTNYQVVCKGEHWVD	60		
APPLICANT: HENRY; MURATA, JUN	QY	DDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIEKLRSCTHSPYMRPVY	206		
TITLE OF INVENTION: MOTILITY STIMULATING	Db	DDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIEKLRSCTHSPYMRPVY	120		
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND	QY	PTKTEPNLYTLTATGLYPESHGIVGNSMYDPVFDATFHLRGREKENHRWWGGQPLWITATK	266		
TITLE OF INVENTION: THERAPY	Db	PTKTEPNLYTLTATGLYPESHGIVGNSMYDPVFDATFHLRGREKENHRWWGGQPLWITATK	180		
NUMBER OF SEQUENCES: 6	QY	QGVKAGTFFWSVSVIPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEES	326		
CORRESPONDENCE ADDRESS:	Db	QGVKAGTFFWSVSVIPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEES	240		
ADDRESSEE: MORGAN & FINNEGAM	QY	SYGSPFTPAKRPKRKVAPKRRQRQERVAPPKKRRKIKHRMDHYAAETRQDKMTNPRLREIDK	386		
STREET: 345 PARK AVENUE	Db	SYGSPFTPAKRPKRKVAPKRRQRQERVAPPKKRRKIKHRMDHYAAETRQDKMTNPRLREIDK	300		
CITY: NEW YORK	QY	IVGQLMDGLKQKLRLRCVNIVFGDGHMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIR	446		
STATE: NEW YORK	Db	IVGQLMDGLKQKLRLRCVNIVFGDGHMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIR	360		
COUNTRY: U.S.A.	QY	SKFSMNAKYDPKAIIANLTCKPDQHEKPYKQHLPKRLHYANNRRIEDHLLVERRWHV	506		
ZIP: 10154	Db	SKFSMNAKYDPKAIIANLTCKPDQHEKPYKQHLPKRLHYANNRRIEDHLLVERRWHV	420		
COMPUTER READABLE FORM:	QY	ARKPLDVYKKPSGKCFQGDHGFNDKVNMSMQTVFGYPTFKYKTPQHDKPQHDKPQHDKP	566		
MEDIUM TYPE: Floppy Disk	Db	ARKPLDVYKKPSGKCFQGDHGFNDKVNMSMQTVFGYPTFKYKTPQHDKPQHDKPQHDKP	480		
COMPUTER: IBM PC compatible	QY	DLLGILKPKAPNNNGTHGSJLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCDKVE	626		
OPERATING SYSTEM: PC-DOS/MS-DOS	Db	DLLGILKPKAPNNNGTHGSJLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDDDLGCTCDKVE	540		
SOFTWARE: WordPerfect 5.1	QY	627 PKNKLDENKRLHTKGSTERHLLYGRPAVLRTYRDILYHTDFESGYSEIFMLLWTSY	686		
CURRENT APPLICATION DATA:	Db	641 PKNKLDENKRLHTKGSTERHLLYGRPAVLRTYRDILYHTDFESGYSEIFMLLWTSY	600		
APPLICATION NUMBER: PCT/US95/06613	QY	687 TVSKQAEVSSVPDHLSCSVRPDVRSFSFSQNCLAYKNDKQMSYGFLEPPYLSSSPEAKY	746		
FILING DATE: 24-MAY-1995	Db	601 TVSKQAEVSSVPDHLSCSVRPDVRSFSFSQNCLAYKNDKQMSYGFLEPPYLSSSPEAKY	660		
CLASSIFICATION:	QY	747 DAFLTNMVPMYPAFKRVWNYFORVLVKKYASERGNVVISGPIFYDYYDGLHDTEDKIK	806		
PRIOR APPLICATION DATA:	QY	7501 QYVEGESSIPVPTHYSITTSCLDFTQADKCDGPLSVSSFILPHRPDNECSNSSEDESK	866		
APPLICATION NUMBER: 08/346,455	Db	761 DAFLVTTNMVPMYPAFKRVWNYFQRVLVKKYASERGNVVISGPIFYDYYDGLHDTEDKIK	720		
FILING DATE: 28-NOV-1994	QY	7801 QYVEGESSIPVPTHYSITTSCLDFTQADKCDGPLSVSSFILPHRPDNECSNSSEDESK	780		
PRIOR APPLICATION DATA:	Db	781 WVEELMKMHTARVRDIEHLSLDFFRKTTSRYPEILTLKTYLHTYESEI	829		
APPLICATION NUMBER: 08/249,182	QY	807 QYVEGESSIPVPTHYSITTSCLDFTQADKCDGPLSVSSFILPHRPDNECSNSSEDESK	866		
FILING DATE: 17-JAN-1992	Db	821 QYVEGESSIPVPTHYSITTSCLDFTQADKCDGPLSVSSFILPHRPDNECSNSSEDESK	780		
ATTORNEY/AGENT INFORMATION:	QY	867 WVEELMKMHTARVRDIEHLSLDFFRKTTSRYPEILTLKTYLHTYESEI	915		
NAME: DOROTHY R. AUTH	Db	881 WVEELMKMHTARVRDIEHLSLDFFRKTTSRYPEILTLKTYLHTYESEI	829		
REGISTRATION NUMBER: 36,434	QY	887 WVEELMKMHTARVRDIEHLSLDFFRKTTSRYPEILTLKTYLHTYESEI	829		
TELECOMMUNICATION INFORMATION:	Db	901 WVEELMKMHTARVRDIEHLSLDFFRKTTSRYPEILTLKTYLHTYESEI	829		
TELEPHONE: (212) 758-4800	QY	921 QYVEGESSIPVPTHYSITTSCLDFTQADKCDGPLSVSSFILPHRPDNECSNSSEDESK	866		
TELEFAX: (212) 751-6849	Db	941 QYVEGESSIPVPTHYSITTSCLDFTQADKCDGPLSVSSFILPHRPDNECSNSSEDESK	780		
INFORMATION FOR SEQ ID NO: 34:	QY	961 QYVEGESSIPVPTHYSITTSCLDFTQADKCDGPLSVSSFILPHRPDNECSNSSEDESK	780		
SEQUENCE CHARACTERISTICS:	Db	981 WVEELMKMHTARVRDIEHLSLDFFRKTTSRYPEILTLKTYLHTYESEI	829		
LENGTH: 829	QY	987 WVEELMKMHTARVRDIEHLSLDFFRKTTSRYPEILTLKTYLHTYESEI	915		
TYPE: amino acid	Db	US-08-346-455B-67	7	RESULT	7
STRANDEDNESS: single		; Sequence 67, Application US/08346455B			
TOPOLOGY: Unknown					
MOLECULE TYPE: protein					
HYPOTHETICAL: No					
ORIGINAL SOURCE:					
ORGANISM: Human					
STRAIN:					
INDIVIDUAL ISOLATE:					
DEVELOPMENTAL STAGE:					
HAPLOTYPE:					
TISSUE TYPE:					
CELL TYPE: Melanoma					
CELL LINE: A2058					
ORGANELLE:					

Patent No. 5731167
 GENERAL INFORMATION:
 APPLICANT: UNITED STATES OF AMERICA; DEPT.
 OF HEALTH AND HUMAN SERVICES
 TITLE OF INVENTION: MOTILITY STIMULATING
 PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 SEQUENCE CHARACTERISTICS:
 LENGTH: 861
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: N-tera 2D1 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 US-08-346-455B-67

Query Match Score 4418; DB 1; Length 861;
 Best Local Similarity 89.0%; Pred. No. 0;
 Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

QY	1	MARRSSFOSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWNTNISGCK	60
Db	1	MARRSSFOSCQIISLFTFAVGVNICLGFTAHRIKRAEGWEEGPPTVLSDSPWNTNISGCK	60
QY	61	GRCFELQEAGPPDCRCNDLCKSYTSCCHDFDECLKTARGWECTKDRGEVRNEENACHC	120
Db	61	GRCFELQEAGPPDCRCNDLCKSYTSCCHDFDECLKTARAWECTKDRGEVRNEENACHC	120
QY	121	SEDECLARGDCCCTNYQVVCKGESEHWWDDCEEEKAACCPAGFVRPLIIFSVDGFRASYMK	180
Db	121	SEDECLARGDCCCTNYQVVCKGESEHWWDDCEEEKAACCPAGEVRPLIIFSVDGFRASYMK	180
QY	181	KGSKVMPIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHIVGNSMYDPVFDA	240

RESULT 8
 US-08-977-221-67
 Sequence 67, Application US/08977221
 Patent No. 6084069
 GENERAL INFORMATION:
 APPLICANT: UNITED STATES OF AMERICA; DEPT.
 OF HEALTH AND HUMAN SERVICES
 TITLE OF INVENTION: MOTILITY STIMULATING
 PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,221
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 LENGTH: 861
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: N-tera 2D1 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 US-08-977-221-67

Query Match 88.0%; Score 4418; DB 3; Length 861;
 Best Local Similarity 89.1%; Pred. No. 0;
 Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

QY 1 MARRSSFQSCQIISLFLPTFAVGVSICLGFATAHKRAEGWEAGPPTVLSDSPWTNISGSCK 60
 Db 1 MARRSSFQSCQIISLFLPTFAVGVNICLGFATAHKRAEGWEAGPPTVLSDSPWTNISGSCK 60

QY 61 GRCFELQEAGPDPDCRCDNLCKSYTSCTSCCHDFDELCLKTARGWECTKDRCGEVRENEACHC 120
 Db 61 GRCFELQEAGPDPDCRCDNLCKSYTSCTSCCHDFDELCLKTARAWECTKDRCGEVRENEACHC 120

Qy 121 SEDCLARGDCCTNYQVVKGEHWVDDCEEIKAAECPAGFVRPLIIFSVDFRASYMK 180
 Db 121 SEDCLARGDCCTNYQVVKGEHWVDDCEEIKAAECPAGFVRPLIIFSVDFRASYMK 180

QY 181 KGSKVMMPNIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIYGNNSMYDPVFDA 240
 Db 181 KGSKVMMPNIEKLRSCTGTHSPHMRPVYPTKTFPNLYTLATGLYPESHGIYGNNSMYDPVFDA 240

QY 241 TFHLRGREKENHRWWGGQPLWITATKQGVKAGTFFWSVII---PHERRILTILRWLTLP 296
 Db 241 TFHLRGREKENHRWWGGQPLWITATKQRGES---WNLILVCCHPSRAEILTILQWLTL 296

QY 297 DHER---PSVYAFYSEQPDFSGHKGPFGEESSYGSPTPAKRPKRKVAPKRRQERPV 352
 Db 297 DHERLRSMPISLSNL---ISLDTNMPPGPE-----323

QY 353 APPKKRRRKIHMDHYAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVFVGDH 412
 Db 324 -----MTNPLREIDKIVGQLMDGLKQLKLRRCVNVFVGDH 359

QY 413 GMEDVTCRTRTEFLSNYLTVNDDITLVPGTGLRGRSKFSNNAKYDPKAIIANLTCKKPQDH 472
 Db 360 GMEDVTCRTRTEFLSNYLTVNDDITLVPGTGLG-IRSKFSNNAKYDPKAIIANLTCKKPQDH 418

RESULT 9
 PCT-US95-06613-67
 Sequence 67, Application PC/TUS9506613
 ; GENERAL INFORMATION:
 ; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
 ; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
 ; APPLICANT: HENRY; MURATA, JUN
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06613
 ; FILING DATE: 24-MAY-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/346,455
 ; FILING DATE: 28-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249,182
 ; FILING DATE: 25-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/822,043
 ; FILING DATE: 17-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DOROTHY R. AUTH
 ; REGISTRATION NUMBER: 36,434

REFERENCE/DOCKET NUMBER: 2026-4149US2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:SEQUENCE CHARACTERISTICS:
LENGTH: 861TYPE: amino acid
STRANDEDNESS: singleTOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NOFEATURE: NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-67

Query Match 88.0%; Score 4418; DB 5; Length 861;
 Best Local Similarity 89.1%; Pred. No. 0;
 Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

QY 1 MARRSFOSCQIISLFTAVGVSICLGFTAHRIKRAEGWEEGPPTVILSDSPWNTNISGSCK 60
 Db 1 MARRSFOSCQIISLFTAVGVNICLGFTAHRIKRAEGWEEGPPTVILSDSPWNTNISGSCK 60

QY 61 GRCFELQEAGPPDCRCDNLCKSYTSCTSCCHDFDELCLKTARGWECKDRCGEVRENACHC 120
 Db 61 GRCFELQEAGPPDCRCDNLCKSYTSCTSCCHDFDELCLKTARAWECKDRCGEVRENACHC 120

QY 121 SEDCLARGDCTNYQVVKGESEHWVDDCEEIKAECPPAGFVRPLLIIFSVDGFRASYMK 180
 Db 121 SEDCLARGDCTNYQVVKGESEHWVDDCEEIKAECPPAGFVRPLLIIFSVDGFRASYMK 180

QY 181 KGSKVMPNIEKLRSCTGTHSPYMRPVYPTKTFPONLYTLATGLYPESHGIVGNNSMDPVFDA 240
 Db 181 KGSKVMPNIEKLRSCTGTHSPHMRPVYPTKTFPONLYTLATGLYPESHGIVGNNSMDPVFDA 240

QY 241 TPHLRGREKFNRWWGGQPLWITATKQGVKAGTFFWSVVI----PHERRLTIRWLTL 296
 Db 241 TPHLRGREKFNRWWGGQPLWITATKQRGES---WNILLVCCHPSRAEILTLQWLTL 296

QY 297 DHER---PSVYAFYSEOPDFSGHKYGPFGPEESSYGSPTPAKRPKRVAPKRQRQERVY 352
 Db 297 DHERLRSMPSSILSNSL----ISLDTNMPFGPE----- 323

QY 353 APPKKRRKIHMDHYAAETRDQKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDH 412
 Db 324 ---- 323

QY 413 GMEDVTCDRTEFLSNLYLTNVDDITLVPGLGRIRSKFSNNAKYDPKAIIANLTCKKPQDH 472
 Db 360 GMEDVTCDRTEFLSNLYLTNVDDITLVPGLTG-MTSKFSNNAKYDPKAIIANLTCKKPQDH 418

QY 473 FKPYLKQHLPKRLHYANNRRIEDIHLLYERRWHVARKPLDVYKTPKVKPAPNNGTHGSLNHLRTNTF 532
 Db 419 FKPYLKQHLPKRLHYANNRRIEDIHLLYERRWHVARKPLDVYKTPKVKPAPNNGTHGSLNHLRTNTF 538

QY 533 VNSMQTVFVGYPGIMYLQSDFDLGLKQAPNNGTHGSLNHLRTNTF 592
 Db 479 VNSMQTVFVGYPGIMYLQSDFDLGLKQAPNNGTHGSLNHLRTNTF 538

QY 593 RPTMPEEVTRPNPGIMYLQSDFDLGLKQAPNNGTHGSLNHLRTNTF 652
 Db 539 RPTMPEEVTRPNPGIMYLQSDFDLGLKQAPNNGTHGSLNHLRTNTF 598

QY 653 RPAVLRTTRYDILYHTDEESGYSEIFLMLLWTSTVSKQAEVSSVPDHLTSCVRPDVRS 712
 Db 599 RPAVLRTTRYDILYHTDEESGYSEIFLMLLWTSTVSKQAEVSSVPDHLTSCVRPDVRS 658

QY 713 PSFSQNCLAYKNDKQMSYGFLLFPYLSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVL 772

RESULT 10
 US-08-346-455B-38
 Sequence 38, Application US/08346455B
 ; Patent No. 5731167
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT .
 ; ADDRESS: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/346,455B
 ; FILING DATE: 28-NOV-1994
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06613
 ; FILING DATE: 24-MAY-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/822,043
 ; FILING DATE: 17-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DOROTHY R. AUTH
 ; REGISTRATION NUMBER: 36,434
 ; REFERENCE/DOCKET NUMBER: 2026-4149PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 38:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 979
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: No
 ; ORIGINAL SOURCE:
 ; ORGANISM: Human
 ; STRAIN:
 ; INDIVIDUAL ISOLATE:
 ; DEVELOPMENTAL STAGE:
 ; HAPLOTYPE:

RESULT 11
US-08-977-221-38

Query Match 85.3%; Score 4279; DB 1; Length 979;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

OTHER INFORMATION: putative autotoxin
OTHER INFORMATION: protein sequence from human liver

Query Match 85.3%; Score 4279; DB 1; Length 979;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

QY 1 MARRSSFQSCQQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60
Db 1 MARRSSFQSCQQDISLFTFAVGVNICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60

QY 61 GRCFELQEAGFPDCRCDDNLCKSYTSCCHDFDELCLKTARGWECKKDRCGEVRNEENACHC 120
Db 61 GRCFELQEAGFPDCRCDDNLCKSYTSCCHDFDELCLKTARAWECKKDRCGEVRNEENACHC 120

QY 121 SEDCLARGDCCNYQVVKRGESHWWDDCEIKEAACCPAGFVRPPLIIIFSVDFG--RASY 178
Db 121 SEDCLARGDCCNYQVVKRGESHWWDDCEIKEAACCLQ--VCSPSINHLLRGWLFLMTSY 178

QY 179 MKKGSKVMPNIEKLRSCTHSPMVPVPTKTFPNLYTLATGLYPESHGIVGNNSMYDPVF 238
Db 179 MKKGSKVMPNIEKLRSCTHSPMVPVPTKTFPNLYTLATGLYPESHGIVGNNSMYDPVF 238

QY 239 DATFHRLGREKFNHRWWGGQPLWITATKOGVKAGTFFWSVV-----PHERRLTILRWLT 294
Db 239 DATEHLRGREKFNHRWWGGQPLWITATKORGES-----WNILLVCCCHPSRAEILTILQWL 294

QY 295 LPDHHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPPFTPAKRKRKVAPKRRQERPVAP 354
Db 295 LPDHHERPSVYAFYSEQPDFSGHKHMPFGPE----- 324

QY 355 PKKRRRK1HMDHYAAETRQDKMTNPRLREIDKIVGQLMDGLKQLRKCNRCCNVIFVGDHGM 414
Db 325 -----MTNPLREMHKIVGQLMDGLKQLRKCNRCCNVIFV---ET 359

QY 415 EDVTCD--RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPQDH 472
Db 360 MDGRCHMYRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPQDH 419

QY 473 FKPYLKQHLPKRLHYANRRIEDIHLVERRWHVARKPLDVKKPSGKCFQGDHGFDNK 532
Db 420 FKPYLKQHLPKRLHYANRRIEDIHLVERRWHVARKPLDVKKPSGNAFSRETTAFDNK 479

QY 533 VNSMOTVFGYGPTEKYKTKVPPFENIELYNVMDLGLKPAPEENNTHGSLNHLRTNTF 592
Db 480 VNSMQTVFGYGPTEKYKTKVPPFENIELYNVMDLGLKPAPEENNTHGSLNHLRTNTF 539

QY 593 RPTMPEEVTRPNYPGIMYLQSDFDLGCTCDKVEPKNKLDLNKRLHTKGSTEERHLLYG 652
Db 540 RPTMPEEVTRPNYPGIMYLQSDFDLGCTCDKVEPKNKLDLNKRLHTKGSTEERHLLYG 599

QY 653 RPAVLRYTRYDILYHTDFESGYSEIFMLLWTSYTVSKQAEVSSVPDHLTSVCRPDVRY 711
Db 600 DRPAVLRYTRYDILYHTDFESGYSEIFMLMLWTSYTVSKQAEVSSVPDHLTSVCRPDVRY 659

QY 712 SPSFSQNCLAYKNDKQMSYGFLLFPPYSSPEAKYDAFLVTNMVPMPYPAFKRVWNYFQRV 711
Db 660 SPSFSQNCLAYKNDKQMSYGFLLFPPYSSPEAKYDAFLVTNMVPMPYPAFKRVWNYFQRV 719

QY 772 LVKKYASERNNGVNVISGPPIFYDGLHDTEDKIKQYVEGSSIIPVPTHYSIITSCLDFT 831
Db 720 LVKKYASERNNGVNVISGPPIFYDGLHDTEDKIKQYVEGSSIIPVPTHYSIITSCLDFT 779

QY 832 QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVRDIEHTLSLFFF 891
Db 780 QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVRDIEHTLSLFFF 839

QY 892 RKTTSRSPYEILTLKTYLHTYESEI 915
Db 840 RKTTSRSPYEILTLKTYLHTYESEI 863

GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
Patent No. 6084069

TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992

PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 2026-4149U\$3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849

REFERENCE/DOCKET NUMBER: 36,434
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 979
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
HAPLOTYPE:
TISSUE TYPE: Liver
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:

IDENTIFICATION METHOD:
 OTHER INFORMATION: putative autotoxin
 OTHER INFORMATION: protein sequence from human liver
 US-08-977-221-38

RESULT 12
 PCT-US95-06613-38

Query Match 85.3%; Score 4279; DB 3; Length 979;
 Best Local Similarity 87.1%; Pred. NO. 0;
 Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

QY 1 MARRSSFQSCQIISLFTFAVGVICLGFATAHRIKRAEGWEEGPPTVILSDSPWTNISGSCK 60
 Db 1 MARRSSFQSCQDISLFTFAVGVNICLGFATAHRIKRAEGWEEGPPTVILSDSPWTNISGSCK 60

QY 61 GRCFELQEAAGPPDCRCDNLCKSYTSCHDFDELCLKTARGWECKDRCGEVRNEENACHC 120
 Db 61 GRCFELQEAAGPPDCRCDNLCKSYTSCHDFDELCLKTARAWECKDRCGEVRNEENACHC 120

QY 121 SEDCLARGDCCTNYQVVCKGESHWVDDCEEIKAAECAPAGFVRPLLIIFSVDGF--RASY 178
 Db 121 SEDCLARGDCCTNYQVVCKGESHWVDDCEEIKAAECLQ--VCSPSINHLLRGWLPMTSY 178

QY 179 MKKGSKVMPNIEKLRSCTGTHSPYMPVYPTKTFPNLYTATGLYPESHGIVGNSMYDPVF 238
 Db 179 MKKGSKVMPNIEKLRSCTGTHSPYMPVYPTKTFPNLYTATGLYPESHGIVGNSMYDPVF 238

QY 239 DATFHLRGREKFENHRWGGPLWITATKQGVKAGTFFWSSVI---PHERRILTLRWLT 294
 Db 239 DATEFHLRGREKFENHRWGGPLWITATKQRGES---WNLLVCCHPSPRAEILTILQWLT 294

QY 295 LPDHHERPSVYAFYSEQPDSGHKYCGPFGEPEESYGSPEPTAKPKRKVAPKRQRQRPVAP 354
 Db 295 LPDHHERPSVYAFYSEQPDSGHKHMPFGPE-- 324

Qy 355 PKRRRKIHMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKRLRCVNViFVGHDHGM 414
 Db 325 ----- MTNPLREMHKIVGQLMDGLKQLKRLRCVNViFV-- ET 359

QY 415 EDVTCD--RTEFLSNYLTVNDDITLVPGTGLGRIRSKFSNNAKYDPKAIIANLTCKKPQDH 472
 Db 360 MDGRCHMYRTFLSNYLTVNDDITLVPGTGLGRIRSKFSNNAKYDPKAIIANLTCKKPQDH 419

QY 473 FKPYLKQHLPKRLHYANNRRIEDIHLLYVERRWHVARKPLDVYKKPSKGCKFFQGDHGFDNK 532
 Db 420 FKPYLKQHLPKRLHYANNRRIEDIHLLYVERRWHVARKPLDVYKKPSGNNAFSRETAFDNK 479

QY 533 VNSMOTVFGYGPTEFKYTKVPPFENIELYNVMCDLIGLKPAPEENNTHGSLNHLRNTF 592
 Db 480 VNSMOTVFGYGPTEFKYTKVPPFENIELYNVMCDLIGLKPAPEENNTHGSLNHLRNTF 539

QY 593 RPTMPEEVTRPNYPGIMYLOSDFDLIGCTDDKVEPKNLDELNKLHKGSTEERHLLY 652
 Db 540 RPTMPEEVTRPNYPGIMYLOSDFDLIGCTDDKVEPKNLDELNKLHKGSTEERHLLY 599

QY 653 -RPAVLRYTRDILYHTDFESGYSEIFMLLWTSYTVSKQAEVSSVPDLTSCVRPDVRY 711
 Db 600 DRPAVLRYTRDILYHTDFESGYSEIFMLPLWTSYTVSKQAEVSSVPDLTSCVRPDVRY 659

QY 712 SPSFSQNCLAYKNDKQMSYGFLLFPPYLSSSPEAKYDAFLYTNNMVPMPYPAFKRVWNYFQRV 771
 Db 660 SPSFSQNCLAYKNDKQMSYGFLLFPPYLSSSPEAKYDAFLYTNNMVPMPYPAFKRVWNYFQRV 719

QY 772 LVKYASERNGVNVISGPIDFYDGLHDTEDKIQYVEGSSIPVPTHYSIITSCLDFT 831
 Db 720 LVKYASERNGVNVISGPIDFYDGLHDTEDKIQYVEGSSIPVPTHYSIITSCLDFT 779

QY 832 QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVDIEHTLSLDF 891
 Db 780 QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVDIEHTLSLDF 839

QY 892 RKTRSYPEIILTKYLHTYESEI 915
 Db 840 RKTRSYPEIILTKYLHTYESEI 863

Query Match 85.3%; Score 4279; DB 5; Length 979;

Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

Qy 1 MARRSSFOSCOIIISLFLTFAVGVUSICLGFATAHKRAEGWEGLPPTVLSDSPWTNISGSCK 60
Db 1 MARRSSFOSCOIIISLFLTFAVGVUSICLGFATAHKRAEGWEGLPPTVLSDSPWTNISGSCK 60

Qy 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENACHC 120
Db 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECKDRCGEVRNEENACHC 120

Qy 121 SEDCLARGDCCTNYQVVCKGEHWVDDCEEIRAAECPAGFVRPLIFSVDFG-RASY 178
Db 121 SEDCLARGDCCTNYQVVCKGEHWVDDCEEIRAAECIQL-VCSPSINHLLRGWLPMTSY 178

Qy 179 MKKGSKVMPNIEKLRSCTHSPYMRVYPTKTEPNLYTLATGLYPESHGIVGNNSMYDPVF 238
Db 179 MKKGSKVMPNIEKLRSCTHSPYMRVYPTKTEPNLYTLATGLYPESHGIVGNNSMYDPVF 238

Qy 239 DATEHLRGREKFENHRWWGGQPLWITATKOGVKAGTFFWSVVI---PHERRILTLRLWLT 294
Db 239 DATEHLRGREKFENHRWWGGQPLWITATKQRGES---WNILLVCCHPSRAEILTLQWLWLT 294

Qy 295 LPDHHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPPFTPAKRPKRKVAPKRRQERPVAP 354
Db 295 LPDHHERPSVYAFYSEQPDFSGHKMFGPE-----324

Qy 355 PKKRRRKIHMDHYAAETRQDKMTNPRLREIDKIVGQLMDGLKQLKLRRCVNVIIVGDHGM 414
Db 325 -----324

Qy 415 EDVTCDD-RTEFLSNYLTVNDDITLVPGTGLRGRSKFSNNAKYDPKAIIANLTCKKPQDH 472
Db 360 MDGRCHMYRTEFLSNYLTVNDDITLVPGTGLRGRSKFSNNAKYDPKAIIANLTCKKPQDH 419

Qy 473 FKPYLKQHLPKRHLHYANNNRIEDIHLVERRWHVARKPLDVFYKKPSGKCFQGDHFDNK 532
Db 420 FKPYLKQHLPKRHLHYANNNRIEDIHLVERRWHVARKPLDVFYKKPSGNAFSRETTAFDNK 479

Qy 533 VNSMQTVFVGYPGTFKYKTKVPPFENIELYNVMCDLGLKAPANNGTBGSLNHLLRTNTF 592
Db 480 VNSMQTVFVGYPGTFKYKTKVPPFENIELYNVMCDLGLKAPANNGTBGSLNHLLRTNTF 539

Qy 593 RPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKKNKLDELNKRHLHTKGSTEERHLLYG 652
Db 540 RPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKKNKLDELNKRHLHTKGSTEERHLLYG 599

Qy 653 -RPAYLYRTRYDLYHTDFESGYSEIFMLLWTSYTYSVSKQAEVSSVPDHLTSCVRPDVRY 711
Db 600 DRPAVLYRTRYDLYHTDFESGYSEIFMLPLWTSYTYSVSKQAEVSSVPDHLTSCVRPDVRY 659

Qy 712 SPFSQNCLAYKNDKOMSYGFLFPYLSSSPEAKYDAFLVTNMVPMPYPAFKRVNNYFQRV 771
Db 660 SPFSQNCLAYKNDKOMSYGFLFPYLSSSPEAKYDAFLVTNMVPMPYPAFKRVNNYFQRV 719

Qy 772 LVKKYASERNGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFT 831
Db 720 LVKKYASERNGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFT 779

Qy 832 QPADKCDGPLSVSSFILPHRPDNEECSNSSEDESKWEEELMKMHTARYVDIEHLSLDFF 891
Db 780 QPADKCDGPLSVSSFILPHRPDNEECSNSSEDESKWEEELMKMHTARYVDIEHLSLDFF 839

Qy 892 RKTTSRYPEILTLKTYLHTYESEI 915
Db 840 RKTTSRYPEILTLKTYLHTYESEI 863

RESULT 13
US-08-346-455B-36
; Sequence 36 , Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/066613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: teratocarcinoma
CELL LINE: N-tera 2D1
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: N-tera 2D1 putative
OTHER INFORMATION: ATX protein sequence
US-08-346-455B-36
Query Match 76.5%; Score 3842; DB 1; Length 788;
Best Local Similarity 85.6%; Pred. No. 0; Mismatches 40; Indels 70; Gaps 8;
Matches 727; Conservative 12; Matches 727; Best Local Similarity 85.6%; Pred. No. 0; Mismatches 40; Indels 70; Gaps 8;
Qy 76 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNNEENACHCSEDCLARGDCTNYQ 135
Db 1 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNNEENACHCSEDCLARGDCTNYQ 60

QY 136 VVCKGEHWDDCEEEKAECPAGEVRPLIIFSVDFG--RASYMKKGSKVMPNIEKLR 193
 Db 61 VVCKGEHWDDCEEEKAECLEQ--VDSPSINHLLRGWLPMTSYMKKGSKVMPNIEKLR 118

QY 194 SCGTHSPYMRPVYPTKTFPVLNTLATTGLYPESHGIVGNSMYDPVFDATEFHRLGREKFNR 253
 Db 119 SCGTHSPYMRPVYPTKTFPVLNTLATTGLYPESHGIVGNSMYDPVFDATEFHRLGREKFNR 178

QY 254 WGGQPLWITATKQGVKAGTFFWSVVI----PHERRILTLRWLTLDHERPSVAFYSE 309
 Db 179 WGGQPLWITATKQRGES---WNILLYCCHPSRAEILTLQWLTLDFHERPSVAFYSE 234

QY 310 QPDFSGHKYGPFGPEESSYGSPTPAKRPKRKVAPKRRQERPVAPPKKRRRKIHMDHYA 369
 Db 235 QPDFSGHKHMPFGPE---- 249

QY 370 AETRQDKMTNPPLREIDKIVGQLMDGLKQLKLRCVNVIIFVGDHGMEDVTCF--RTEFLSN 427
 Db 250 ----MNPNPLREMHKIVGQLMDGLKQLKLRCVNVIIF---ETMDGRCHMYRTEFLSN 299

QY 428 YLTINVDDITLVPGTGLRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHY 487
 Db 300 YLTINVDDITLVPGTGLRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHY 359

QY 488 ANNRRIEDHLLVERRWHYARKPLDYYKKPSGKCFQGDHGFDNKVNISMOTVFGYGYGPTF 547
 Db 360 ANNRRIEDHLLVERRWHYARKPLDYYKKPSGNAFPNFSRETTAFDNKVNISMOTVFGYGYGPTF 419

QY 548 KYTKVPPFENIELNVNCMDLGLKPAPNNGTHGSLNHLJRTNTFRPTMPEEVTRPNYPG 607
 Db 420 KYTKVPPFENIELNVNCMDLGLKPAPNNGTHFSLNHLJRTNTFRPTMPEEVTRPNYPG 479

QY 608 IMYQLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTBERHLLYG-RPAVLYRTRYDILY 666
 Db 480 IMYQLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTEERHLLYGDRAVLYRTRYDILY 539

QY 667 HTDFESGYSEIFMLLWTSTVSKQAEVSSVPDHLTSCVRPDVRSPFSQNCLAYKNDK 726
 Db 540 HTDFESGYSEIFMLPLWTSTVSKQAEVSSVPDHLTSCVRPDVRSPFSQNCLAYKNDK 599

QY 727 QMSYGFLLPPYLSPEAKYDAFLVLTNVMVPMYPAFKRVWNYFQRVLVKKYASERGVNVI 786
 Db 600 QMSYGGLGPYLSPEAKYDAFLVLTNVMVPMYPAFKRVWNYFQRVLVKKYASERGVNVI 659

QY 787 SGPIFDDYDGLHDTEDKIKOYVEGSS1PVPTHYSITTSCLDFTOPADKCDGPLSVSSF 846
 Db 660 SGPIFDDYDGLHDTEDKIKOYVEGSS1PVPTHYSITTSCLDFTQPADKCDGPLSVSSF 719

QY 847 ILPHRPDNEECSNSSEDESKEWELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKT 906
 Db 720 ILPHRPDNEECSNSSEDESKEWELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKT 779

QY 907 YLHTYESEI 915
 Db 780 YLHTYESEI 788

RESULT 14
 US-08-977-221-36
 ; Sequence 36, Application US/08977221
 ; Patent No. 6084069
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK

Query Match 76.5%; Score 3842; DB 3; Length 788;
 Best Local Similarity 85.6%; Pred. No. 0;
 Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSYTSCHDFDELCKTARGWECKDRGEVRNEENACHCSEDCDLRGDCCTNYQ 135
 Db 1 CDNLCKSYTSCHDFDELCKTARAWECKDRGEVRNEENACHCSEDCDLRGDCCTNYQ 60

QY 136 WVCKGEHWDDCEEKAECPAGEVRPLIIFSVDFG--RASYMKKGSKVMPNIEKLR 193
 Db 61 WVCKGEHWDDCEEKAECLEQ--VDSPSINHLLRGWLPMTSYMKKGSKVMPNIEKLR 118

QY 194 SCGTHSPYMRPVYPTKTFPONLYTLATGLYPESHIVGNSMYDPVFDATEFHRLGREKFNR 253
 Db 119 SCGTHSPYMRPVYPTKTFPONLYTLATGLYPESHIVGNSMYDPVFDATEFHRLGREKFNR 178

QY 254 WGGQPLWITATKOGVKAGTFFWSVVI----PHERRILTLRWLTLDHERPSVYAFYSE 309
 Db 179 WGGQPLWITATKORGES---WNILVCCHPSRAEILTLQWLTLDFHERPSVYAFYSE 234

RESULT 15
PCT-US95-06613-36
; Sequence 36, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:

QY 310 QPDFSGHKYGPFGPEESSYGSPTPAKRPKRKVAPKRRQERPVA
PPKKRQRRKTHRMDHYA 369
Db 235 QPDFSGHKHMPFGPE----- 249

QY 370 AETRQDKMTNPLREIDKIVGQLMDGLKOLKLRRCVNVIFVGDHGMEDVTCD--RTEFLSN 427
Db 250 ---MPNPLREMHKIVGQLMDGLKOLKLRRCVNVIFV--ETMDGRCHMYRTEFLSN 299

QY 428 YLTNVDDITLVPGLTGRIRSKFSNNAKYDPKAIIANLTCKPKDQHFKPYLKQHLPRKLHY 487
Db 300 YLTNVDDITLVPGLTGRIRSKFSNNAKYDPKAIIANLTCKPKDQHFKPYLKQHLPRKLHY 359

QY 488 ANNRRIEDIHLLVERRWAVARKPLDWYKPKPSGKCFQGDHGFDNKVNSMOTVFVGYGPTF 547
Db 360 ANNRRIEDIHLLVERRWAVARKPLDWYKPKPSGNAFSRETTAFDNKVNSMOTVFVGYGPTF 419

QY 548 KYKTkvppfenielxnyMCDLGLKpapnngthslnhllrtntfrptmpeevtrpnyPG 607
Db 420 KYKTkvppfenielxnyMCDLGLKpapnngthslnhllrtntfrptmpeevtrpnyPG 479

QY 608 IMYLQSDFDLGTCDDKVEPKNKLDELNKRLHTKGSTEERHLLYGRPAVLRTTRYDILY 666
Db 480 IMYLQSDFDLGTCDDKVEPKNKLDELNKRLHTKGSTEERHLLYGRPAVLRTTRYDILY 539

QY 667 HTDFESEGYSEIFFLMLLWTSYTYSKQAEVSSVPDHLTSCVRPDSFSQNCLAYKNDK 726
Db 540 HTDFESEGYSEIFFLMLLWTSYTYSKQAEVSSVPDHLTSCVRPDSFSQNCLAYKNDK 599

QY 727 QMSYGFLLFPYPLSSSPEAKYDAFLVTNMVPMPYPAFKRVWNYFQRVLVKKYASERNGVNV 786
Db 600 QMSYGGGLGPPYPLSSSPEAKYDAFLVTNMVPMPYPAFKRVWNYFQRVLVKKYASERNGVNV 659

QY 787 SGPIFDDYDGHLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTQPADKCDGPLSVSSF 846
Db 660 SGPIFDDYDGHLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTQPADKCDGPLSVSSF 719

QY 847 ILPHRPDNEESCNSSDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEELTLKT 906
Db 720 ILPHRPDNEESCNSSDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEELTLKT 779

QY 907 YLHTYESEI 915
Db 780 YLHTYESEI 788

Query Match 76.5%; Score 3842; DB 5; Length 788;
Best Local Similarity 85.6%; Pred. NO. 0;
Matches 727; conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRENNEAHCSEDCLARGDCCTNYQ 135
Db 1 CDNLCKSYTSCCHDFDELCLKTARAWECTKDRCGEVRENNEAHCSEDCLARGDCCTNYQ 60

QY 136 VVCKGEHWWDDCEEIKAAECPAGFVRPPLIIFSVDFG--RASYMKKGSKVMPNIKLR 193
Db 61 VVCKGEHWWDDCEEIKAAECLO--VDSPSINHLLRGWLPMNTSYMKKGSKVMPNIKLR 118

QY 194 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYPDVFDATFLRGREKFNHR 253
Db 119 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYPDVFDATFLRGREKFNHR 178

QY 254 WMGGQPLWITATQGVKAGFFFWSVVI---PHERRILTILRWLTPDHRSVYAFYSE 309
Db 179 WWAGQPLWITATKORGES---WNILLVCCHPSRAEILTLQWLTLPDHRSVYAFYSE 234

QY 310 QPDFSGHKYGPFGPEESSYGSPTPAKRPKRKVAPKRRQERPVA
PPKKRQRRKTHRMDHYA 369
Db 235 QPDFSGHKHMPFGPE----- 249

QY 370 AETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCNVIFVGDHGMEDVTCD--RTEFLSN 427
Db 250 ---MPNPLREMHKIVGQLMDGLKQLKLRRCNVIFV--ETMDGRCHMYRTEFLSN 299

QY 428 YLTNVDDITLVPGLTGRIRSKFSNNAKYDPKAIIANLTCKKKPDKQHFKPYLKQHLPRKLHY 487

Db	300	YLTNVDDITLVPGTLGRIRSKFSNNAKYDPKALLIANLTCKKPDQHFKPYLKQHLPKRLHY	359
Qy	488	ANNRRIEDIHLVERRWIVARKPLDYYKKPSGKCFQGDHGFDNKVNSMOTVFVGYGPTF	547
Db	360	ANNRRIEDIHLVERRWIVARKPLDYYKKPSGNAFSRETTAFDNKVNSMOTVFVGYGPTF	419
Qy	548	KYTKVPPFENIELYVMCDLGLKAPANNNGTHGSNLNHLRNTFRPTMPEEVTRPNYPG	607
Db	420	KYTKVPPFENIELYVMCDLGLKAPANNNGTHFSNLNHLRNTFRPTMPEEVTRPNYPG	479
Qy	608	IMYLQSDFDLGLCTCDDKVEPKNKLDELNLKRHTKGSTEERHLLYGRPAVLYRTRYDILY	666
Db	480	IMYLQSDFDLGLCTCDDKVEPKNKLDELNLKRHTKGSTEERHLLYGRPAVLYRTRYDILY	539
Qy	667	HTDFESGYSEIFLMLLWTSTVSKQAEVSSVPDHLTSCVRPDYRVSPSFSONCLAYKNDK	726
Db	540	HTDFESGYSEIFLMLPLWTSTVSKQAEVSSVPDHLTSCVRPDYRVSPSFSONCLAYKNDK	599
Qy	727	QMSYGFIFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLYKKYASERGVNV	786
Db	600	QMSYGGLGPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLYKKYASERGVNV	659
Qy	787	SGPIFDDYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTOPADKCDGPLSVSSF	846
Db	660	SGPIFDDYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTOPADKCDGPLSVSSF	719
Qy	847	ILPHRPDNEECSNSSEDESKWEELMKMHATARVDIEHLTSLDFFRKTSRSYPEILTLKT	906
Db	720	ILPHRPDNEECSNSSEDESKWEELMKMHATARVDIEHLTSLDFFRKTSRSYPEILTLKT	779
Qy	907	YLHTYESEI 915	
Db	780	YLHTYESEI 788	

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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:26 ; Search time 20.45 Seconds
 (without alignments)
 12.806 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
 Sequence: 1 YMRRPVYPTKTFPN 13

Perfect score: 76

Sequence: BLOSUM62
 Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	76	100.0	788	1 US-08-346-455B-36	Sequence 36, Appl
2	76	100.0	788	3 US-08-977-221-36	Sequence 36, Appl
3	76	100.0	788	5 PCT-US95-06613-36	Sequence 36, Appl
4	76	100.0	829	1 US-08-346-455B-34	Sequence 34, Appl
5	76	100.0	829	3 US-08-977-221-34	Sequence 34, Appl
6	76	100.0	829	5 PCT-US95-06613-34	Sequence 34, Appl
7	76	100.0	915	1 US-08-346-455B-69	Sequence 69, Appl
8	76	100.0	915	3 US-08-977-221-69	Sequence 69, Appl
9	76	100.0	915	5 PCT-US95-06613-69	Sequence 69, Appl
10	76	100.0	979	1 US-08-346-455B-38	Sequence 38, Appl
11	76	100.0	979	3 US-08-977-221-38	Sequence 38, Appl
12	76	100.0	979	5 PCT-US95-06613-38	Sequence 38, Appl
13	71	93.4	861	1 US-08-346-455B-67	Sequence 67, Appl
14	71	93.4	861	3 US-08-977-221-67	Sequence 67, Appl
15	71	93.4	861	5 PCT-US95-06613-67	Sequence 67, Appl
16	69	90.8	873	3 US-09-187-331-6	Sequence 6, Appl
17	69	90.8	925	2 US-08-392-946-1	Sequence 1, Appl
18	69	90.8	925	2 US-08-504-169-1	Sequence 1, Appl
19	69	90.8	925	5 PCT-US94-14893-1	Sequence 1, Appl
20	40	52.6	203	2 US-08-684-024-8	Sequence 8, Appl
21	40	52.6	203	3 US-09-145-868-8	Sequence 8, Appl
22	40	52.6	205	2 US-08-684-024-1	Sequence 1, Appl
23	40	52.6	205	2 US-08-684-024-6	Sequence 6, Appl
24	40	52.6	205	2 US-08-684-024-7	Sequence 7, Appl
25	40	52.6	205	3 US-09-145-868-1	Sequence 1, Appl
26	40	52.6	205	3 US-09-145-868-6	Sequence 6, Appl
27	40	52.6	205	3 US-09-145-868-7	Sequence 7, Appl

RESULT 1
 US-08-346-455B-36
 ; Sequence 36, Application US/08346455B
 ; Patent No. 5731167
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 788
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein

HYPOTHETICAL: No
 ORIGINAL SOURCE: Human
 STRAIN: N-tera 2D1
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE: teratocarcinoma
 CELL LINE: N-tera 2D1
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: N-tera 2D1 putative ATX protein sequence US-08-4546-455B-36

Query Match 100.0%; Score 76; DB 1; Length 788;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRFVYPTKTFPN 13
 Db 126 YMRFVYPTKTFPN 138

RESULT²
 US-08-977-221-36
 Sequence 36, Application US/08977221
 Patent No. 6084069

GENERAL INFORMATION:
 APPLICANT: UNITED STATES OF AMERICA; DEPT.
 APPLICANT: OF HEALTH AND HUMAN SERVICES
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 TITLE OF INVENTION: THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,221
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
 LENGTH: 788
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE: teratocarcinoma
 CELL LINE: N-tera 2D1
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: N-tera 2D1 putative ATX protein sequence US-08-977-221-36

Query Match 100.0%; Score 76; DB 3; Length 788;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRFVYPTKTFPN 13
 Db 126 YMRFVYPTKTFPN 138

RESULT³
 PCT-US95-06613-36
 Sequence 36, Application PC/TUS9506613
 GENERAL INFORMATION:
 APPLICANT: STRAKE, MARY; LIOTTA, LANCE;
 APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
 APPLICANT: HENRY; MURATA, JUN
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 TITLE OF INVENTION: THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,221
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 36:

REGISTRATION NUMBER: 36,434
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 788
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: teratocarcinoma
 CELL LINE: N-tera 2D1
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: N-tera 2D1 putative
 OTHER INFORMATION: ATX protein sequence
 PCT-US95-06613-36

Query Match 100.0%; Score 76; DB 5; Length 788;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4 US-08-346-455B-34
 ; Sequence 34, Application US/08346455B
 ; Patent No. 5731167
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182

FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 829
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: Putative protein
 OTHER INFORMATION: sequence of A2058 Autotaxin
 US-08-346-455B-34

Query Match 100.0%; Score 76; DB 1; Length 829;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 5 US-08-977-221-34
 ; Sequence 34, Application US/08977221
 ; Patent No. 6084069
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,221
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994

PRIOR APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994

PRIOR APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992

ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH

REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US3

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 829

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown

MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human

STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:

TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: Putative protein sequence of A2058 Autotaxin
 US-08-977-221-34

Query Match 100.0%; Score 76; DB 3; Length 829;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 Db 115 YMRPVYPTKTFPN 127

RESULT 6 PCT-US95-06613-34
 Sequence 34, Application PC/TUS9506613
 GENERAL INFORMATION:
 APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
 APPLICANT: HENRY; MURATA, JUN
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 TITLE OF INVENTION: THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 829
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: Putative protein sequence of A2058 Autotaxin
 PCT-US95-06613-34

Query Match 100.0%; Score 76; DB 5; Length 829;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 Db 115 YMRPVYPTKTFPN 127

RESULT 7 US-08-346-455B-69
 Sequence 69, Application US/08346455B
 GENERAL INFORMATION:
 APPLICANT: UNITED STATES OF AMERICA; DEPT.
 APPLICANT: OF HEALTH AND HUMAN SERVICES
 Patent No. 5731167
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk

CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 36,434
 FILING DATE: 17-JAN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992

PRIOR APPLICATION DATA:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 2026-4149US3
 REFERENCE/DOCKET NUMBER: 2026-4149PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 915
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: A2058 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 US-08-977-221-69

Query Match 100.0%; Score 76; DB 3; Length 915;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 PCT-US95-06613-69
 Sequence 69, Application PC/TUS9506613

GENERAL INFORMATION:
 APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
 APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
 APPLICANT: HENRY; MURATA, JUN
 TITLE OF INVENTION: MOTILITY STIMULATING
 PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 THERAPY
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/066613
 FILING DATE: 24-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/346,455

FILING DATE: 28-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/249,182

FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/822,043

FILING DATE: 17-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: DOROTHY R. AUTH

REGISTRATION NUMBER: 36,434

REFERENCE/DOCKET NUMBER: 2026-4149US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 915

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Unknown

MOLECULE TYPE: CDNA

HYPOTHETICAL: No

FEATURE:

NAME/KEY: A2058 ATX protein

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PCT-US95-06613-69

Query Match 100.0%; Score 76; DB 5; Length 915;
 Best Local Similarity 100.0%; Fred. No. 0.00013;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10

US-08-346-455B-38

Sequence 38, Application US/08346455B

Patent No. 5731167

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT .

APPLICANT: OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: MOTILITY STIMULATING

TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: U.S.A.

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/346,455B

FILING DATE: 28-NOV-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06613

FILING DATE: 24-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 979
 TYPE: amino acid
 STRANDEDNESS: single
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE: Liver
 CELL TYPE:
 CELL LINE:
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: putative autotaxin
 OTHER INFORMATION: protein sequence from human liver
 US-08-346-455B-38

Query Match 100.0%; Score 76; DB 1; Length 979;
 Best Local Similarity 100.0%; Fred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

US-08-977-221-38

Sequence 38, Application US/08977221

Patent No. 6084069

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT .

APPLICANT: OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: MOTILITY STIMULATING

TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: U.S.A.

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,221
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 979

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE: Liver
 CELL TYPE:
 CELL LINE:
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: putative autotaxin
 OTHER INFORMATION: protein sequence from human liver
 US-08-977-221-38

Query Match 100.0%; Score 76; DB 3; Length 979;
 Best Local Similarity 100.0%; Pred. No. 0.00014; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 PCT-US95-06613-38
 Sequence 38, Application PC/TUS9506613
 GENERAL INFORMATION:
 APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
 APPLICANT: SCHIFFMANN, ELLIOT; KRUTZSCH,
 APPLICANT: HENRY; MURATA, JUN
 TITLE OF INVENTION: MOTILITY STIMULATING
 PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 THERAPY
 NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.

ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 979
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE: Liver
 CELL TYPE:
 CELL LINE:
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: putative autotaxin
 OTHER INFORMATION: protein sequence from human liver
 PCT-US95-06613-38

Query Match 100.0%; Score 76; DB 5; Length 979;
 Best Local Similarity 100.0%; Pred. No. 0.00014; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 US-08-346-455B-67
 Sequence 67, Application US/08346455B
 GENERAL INFORMATION:
 Patent No. 5731167

Db 201 YMRPVYPTKTFPN 213

Query Match 100.0%; Score 76; DB 5; Length 979;
 Best Local Similarity 100.0%; Pred. No. 0.00014; Mismatches 0; Indels 0; Gaps 0;

Db 201 YMRPVYPTKTFPN 213

RESULT 13
 US-08-346-455B-67
 Sequence 67, Application US/08346455B
 GENERAL INFORMATION:
 APPLICANT: UNITED STATES OF AMERICA; DEPT.
 APPLICANT: OF HEALTH AND HUMAN SERVICES
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 THERAPY
 NUMBER OF SEQUENCES: 69

Correspondence Address:
 Addressee: MORGAN & FINNEGAN
 Street: 345 PARK AVENUE
 City: NEW YORK
 State: NEW YORK
 Country: U.S.A.

Number of Sequences: 69

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/346,455B
 FILING DATE: 28-NOV-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 861
 NAME/KEY: N-tera 2D1 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 US-08-346-455B-67

Query Match 93.4%; Score 71; DB 1; Length 861;
 Best Local Similarity 92.3%; Pred. No. 0.00079; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 US-08-977-221-67
 ; Sequence 67, Application US/08977221
 ; Patent No. 6084069
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT. OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992

ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751 6849
INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-67

Query Match 93.4%; Score 71; DB 5; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YMRRPVYPTKTFPN 13
Db 201 HMRPVYPTKTFPN 213

Search completed: July 19, 2001, 14:45:27
Job time: 180 sec

GenCore version 4.5
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QTM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:22 ; Search time 25.97 Seconds
(without alignments)
2683.855 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSSFQSCQIISLFTFAV. RSYPEILTLKTYLHTYESEI 915

BLOSUM62
Gapext 0.5

Scoring table:

Searched: 319241 segs; 76174552 residues

Total number of hits satisfying chosen parameters: 210241

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

MaxLink Match 100%
Listing first 15 summaries

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1:     -pir1:*
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P-112: *
BijF3: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	915	1 A55144	autotaxin precursor
2	4306	85.8	885	1 A55453	plasma cell membra
3	2084	41.5	875	1 A57080	cell surface antig
4	1955.5	39.0	925	1 A39216	plasma cell membra
5	1899.5	37.8	905	1 A27410	plasma cell membra
6	646.5	12.9	457	2 T09932	nucleotide pyropho
7	612	12.2	496	2 T09931	nucleotide pyropho
8	611.5	12.2	479	2 T03293	nucleotide pyropho
9	610	12.2	829	2 T19494	probable phosphodie
10	609	12.1	461	2 T09933	hypothetical prote
11	539.5	10.7	485	2 T40657	phosphodiesterase-
12	522	10.4	429	2 T33724	hypothetical prote
13	461	9.2	433	2 B82537	hypothetical prote
14	456.5	9.1	674	2 T19495	protein kinase PC-
15	456	9.1	300	2 A41179	hypothetical prote
16	410	8.2	743	2 S19437	hypothetical prote
17	335.5	6.7	493	2 S50443	hypothetical prote
18	297.5	5.9	614	2 T30973	hypothetical prote
19	241.5	4.8	133	2 T09934	hypothetical prote
20	238	4.7	96	2 A25274	phosphodiesterase
21	238	4.7	453	2 T16795	hypothetical prote
22	163	3.2	360	2 T20867	hypothetical prote
23	146.5	2.9	329	1 NCBYNI	nuclease NUC1 (EC
24	145.5	2.9	465	2 T34936	hypothetical prote
25	142	2.8	1186	2 T03180	tyrosine protein k
26	132	2.6	462	2 T36185	hypothetical prote
27	127	2.5	1820	2 A55494	latent transformin
28	123.5	2.5	454	2 A46498	glucocorticoid-sen
29	122	2.4	1374	2 A70712	protein-tirosino

A; Reference number: A42329; MUID: 92129337
A; Accession: A42329
A; Molecule type: protein
A; Residues: 256-266;422-444;504-507,'AN';510,'X',511-515;533-548;'S',554-559,'N',561-
A; Experimental source: A2058 melanoma cells
A; Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A; Note: a peptide fragment Tyr-Asp-Val-Pro-Trp-Asn-Glu-Thr-Ile was also found
C; Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
C; Genetics:
A; Gene: GDB:ATX
A; Cross-references: GDB: 378346
A; Map position: 8q22-8qter
C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C; Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
F; 55-98/Domain: somatomedin B homology <SBH1>
F; 99-142/Domain: somatomedin B homology <SBH2>
F; 54, 463, 577, 859/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 210/Binding site: AMP (Thr) (covalent) #status predicted

Query	Match	Score	Length	
	100.0%	5019	915;	
Best Local Similarity	100.0%	Pred. No.	0;	
Matches	915;	Conservative	0;	
	Mismatches	0;	Indels	0;
	Gaps	0;		
QY	1 MARRSSFQSQQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK	60		
Db	1 MARRSSFQSQQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK	60		
QY	61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC	120		
Db	61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC	120		
QY	121 SEDCLABCDGCTTNWQVWQVCEGCUWDDCEEEWAAEDACTWDPLIBSUDCDDGUM	180		

		A; Description: Cloning and expression of brain-specific nucleotide diphosphohydrolase
		A; Reference number: JU0187
		A; Accession: JU0187
		A; Molecule type: mRNA
		A; Residues: 1-66, 'O', 68-81, 'T', 83-94, 'C', 96, 'A', 98-195, 'A', 197-514, 'E', 516-621, 'E', 62
		A; Experimental source: strain Sprague-Dawley
		C; Superfamily: nucleotide pyrophosphatase: somatomedin B homology
		C; Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester
		F; 54-97/Domain: somatomedin B homology <SBH1>
		F; 98-141/Domain: somatomedin B homology <SBH2>
		F; 53,150,396,408,522,608,829/Binding site: carbohydrate (Asn) (covalent) #status pred
		F; 207/Binding site: AMP (Thr) (covalent) #status predicted
		Query Match 85.8%; Score 4306; DB 1; Length 885;
		Best Local Similarity 83.6%; Pred. No. 1.7e-287;
		Matches 792; Conservative 33; Mismatches 28; Indels 94; Gaps 6;
QY	181	KGSKVMMPNIEKLRSQCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY	181	KGSKVMMPNIEKLRSQCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db	181	KGSKVMMPNIEKLRSQCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
QY	241	TFHLRGREKFNRHRWGGQPLWITATKQGVKAGTFFWSSVIPHERRILTLRLWLTPDHER 300
Db	241	TFHLRGREKFNRHRWGGQPLWITATKQGVKAGTFFWSSVIPHERRILTLRLWLTPDHER 300
QY	301	PSVYAFYSEQPQDFSGHKYGPFGPEESSYGSPTPAARRPKRKVAPKRQERPVAPPKKRRR 360
Db	301	PSVYAFYSEQPQDFSGHKYGPFGPEESSYGSPTPAAKPKRKVAPKRQERPVAPPKKRRR 360
Db	361	KIHRMDHYAAETRQDKMTNPRLREIDKIVGQLMDGIKQLKLRRRCVNVIFFYGDHMEDVTCD 420
Db	361	KIHRMDHYAAETRQDKMTNPRLREIDKIVGQLMDGIKQLKLRRRCVNVIFFYGDHMEDVTCD 420
QY	421	RTEELSNYLTVDDITLVPGLTRGRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQH 480
Db	421	RTEELSNYLTVDDITLVPGLTRGRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQH 480
QY	481	LPKRLYANNRRIEDIHLVERRWHARKPLDVKPPFENIELYNVMCDLLGLKAPAPNGTHGSNLHLLRTNTFRPTMPEEV 540
Db	481	LPKRLYANNRRIEDIHLVERRWHARKPLDVKPPFENIELYNVMCDLLGLKAPAPNGTHGSNLHLLRTNTFRPTMPEEV 540
QY	541	VGYGPTFKYKTKVPPFENIELYNVMCDLLGLKAPAPNGTHGSNLHLLRTNTFRPTMPEEV 600
Db	541	VGYGPTFKYKTKVPPFENIELYNVMCDLLGLKAPAPNGTHGSNLHLLRTNTFRPTMPEEV 600
QY	601	TRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDDELNRKLHTKGSTEERHLLYGRPAVLRT 660
Db	601	TRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDDELNRKLHTKGSTEERHLLYGRPAVLRT 660
QY	661	RYDILYHTDFESGYSEIFMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRSPSFSQNCL 720
Db	661	RYDILYHTDFESGYSEIFMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRSPSFSQNCL 720
QY	721	AYKNDKOMSYGFLLFPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLVKKYASER 780
Db	721	AYKNDKOMSYGFLLFPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLVKKYASER 780
QY	781	NGVNVISGPIDFYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTQPADKCDGP 840
Db	781	NGVNVISGPIDFYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTQPADKCDGP 840
QY	841	LSVSSFILPHRDNEECSNSSEDESKWVEELMKMHTARVRDIEHTSCLDFTQPADKCDGP 840
Db	841	LSVSSFILPHRDNEECSNSSEDESKWVEELMKMHTARVRDIEHTSCLDFTQPADKCDGP 840
QY	901	ILTIKTYLHTYESEI 915
Db	901	ILTIKTYLHTYESEI 915
RESULT 2		
A55453		plasma cell membrane glycoprotein PC-1, brain specific - rat
		N; Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
		C; Species: Rattus norvegicus (Norway rat)
		C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
		C; Accession: A55453; JU0187
		R; Narita, M.; Goji, J.; Nakamura, H.; Sano, K.
		J. Biol. Chem. 269, 28235-28242, 1994
		A; Title: Molecular cloning, expression, and localization of a brain-specific phosphodiesterase
		A; Reference number: A55453; MUID:95050605
		A; Molecule type: mRNA
		A; Residues: 1-885 <NAR>
		A; Cross-references: GB:D28560; NID:9464196; PID:BAA05910.1; PID:9464197
		R; Narita, M.; Goji, J.; Sano, K.; Nakamura, H.
		submitted to JIPID, February 1994
		Db 719 FLVTNMVPMYPAFKRVWAYFORVLVKYASERNGVNVISGPIDFYDGLHDTEDKIKQY 778

QY 809 VEGSSIPVPTHYSIITSCLDFTQPADKCDGFLSVSSFILPHRPDNEESCNSSDESKWV 868
 Db 779 VEGSSIPVPTHYSIITSCLDFTQPADKCDGFLSVSSFILPHRPDNEESCNSSDESKWV 838

QY 869 EELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTILKTYLHTYESEI 915
 Db 839 EELMKMHTARVRDIEHLTGLDFYRKTSRSYSEILTILKTYLHTYESEI 885

RESULT 3

A57080 cell surface antigen RB13-6 - rat
 N; Contains: Phosphodiesterase I (EC 3.1.4.1)
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C; Accession: A57080
 R; Deissler, H.; Lottspeich, F.; Rajewsky, M.F.
 J. Biol. Chem. 270, 9849-9855, 1995
 A; Title: Affinity purification and cDNA cloning of rat neural differentiation and tumor
 A; Reference number: A57080; MUID:95247775
 A; Accession: A57080
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-875 <DEI>
 A; Cross-references: GB:247987; NID:9806378; PIDN:CAA88029.1; PID:g806379
 C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology
 C; Keywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase; sur
 F; 1-22/Domain: cytosolic #status predicted <CYT>
 F; 23-45/Domain: transmembrane #status predicted <TMM>
 F; 46-875/Domain: extracellular #status predicted <EXT>
 F; 51-94/Domain: somatomedin B homology <SBH>
 F; 95-138/Domain: somatomedin B homology <SBH2>
 F; 206/Binding site: AMP (Thr) (covalent) #status predicted
 F; 237,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status pr
 A; Residues: 1-875 <DEI>

Query Match 41.5%; Score 2084; DB 1; Length 875;
 Best Local Similarity 43.5%; Pred. No. 5e-135;
 Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;

QY 57 GSCKGRCFELQEAGPPDCRCDNLCKSYTSCCCHDFDELCLKTARGWECKDKRCGEVRNEEN 116
 Db 53 GSCRKKCFDSHRLGCRCDSGCTDRGDCCWDFFEDTCVKSTQIWTONSFRCGETRLEAA 112

QY 117 ACHCSEDCLARGDCCTNYQVVCKGEHWVDDCEEIAKAECPAGFVRPPLIIFSVDFGRA 176
 Db 113 LCSCADDCLQRKDCCDTDYKAVCQGEWPWVTEACASSQEPQCPEGFDQPPVILFSMDGFR 172

QY 177 SYMKKGSKYMPNTEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIYGNMSYDP 236
 Db 173 EYLQTWSTLLPNINKLKTKCGLHSKYMRAAMYPTKTFPNHYTIVTGLYPESHGIIDNNMYDV 232

QY 237 VFDATEFHLRGREKFNRWLTLDHERPSVAFYSEQPDFSGHKGKYGPGPEESSYGSPPFTPAKRP 338
 Db 233 YLNKNFSSLSSVEKSNPAAWSGQPIWLTAMYQGLKAASYYWLGSDVAVNGSFNPNIYRYSN 292

QY 279 VIPHERRILTLRWLTLDHERPSVAFYSEQPDFSGHKGKYGPGPEESSYGSPPFTPAKRP 338
 Db 293 SVPYESRIATLQLWDLKERAERPSFTIYVEEPDSAGHKSGPV-----SAG----- 338

QY 339 KRKVAPKRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPRLREIDKIVGOLMDGLKQL 398
 Db 339 -----VIKALQLVDAFGMLMEGLKQR 360

QY 399 KLRCRVNVIFYGDHGMEDVTCDRTEFLSNYLTVNDDITLWPGTGLGRISK-----FSNN 452
 Db 361 NLHNHCVNIIIVLAHDHGMDDQTISCDRVEYMTDYFPEI-NFYMYQQGPAPRIRTRNIPQDFFTIN 419

QY 453 AKYDPKAIANLTCKRPDQHFKPYLKQHLPLKRLHYANNRRIEIDIHLVERRWHAARKPLD 512

Db 420 S---EEIVRDLSCRKSDQHFKPYLTPDLPKRLHYAKNVRIDKVLHMVDROWLAYR---- 471

Db 529 PAPNGSHGSLNHLKAPFYOPSHAELSKSAGCGFTTPLPKDSLNCSC-LALOTSGQEE 587

QY 633 ELNKRLHTKG---STEERHLLYGRPAVLRYTR-YDLYHTDFESGYSEIIFMLLWTSYT 687
 Db 588 QVNQRLNLNSGGEVSAEKTNLPFGRPRVIQQNKNKDHCCLLYHREYVSGFGKAMKMPMWSSYT 647

QY 688 VSKQAEVSSVPDHLTSCVRPDVSPFSQNCLAYKNDQMSYGFLLFPYLSSSPEAKYD 747
 Db 648 VPKPQGDTSSLPLPTVPDFCLRADVRVDPSESQKCSFYLADQNIIDHGFLYPAIKGNNEQSYD 707

QY 748 AFLVTNNKVPMYPAFKRVWNYFORVVLVKKYASERGVNVISGPPIFDYDYGGLHDTEDKIKQ 807
 Db 708 ALITSNLVPMYKEFKMWDYFHKVULLKYYAIERNGVNVSQSPPIFDYNYDGHFDAPEITN 767

QY 808 YVEGSSIPVPTHYSTLTSCLDFTQPADKCDGFLSVSSFILPHRPDNEESCSSEDESKW 867
 Db 768 YVAGTDVVPVPHYFVVLTSCKNKTHTPDSCPGLDVLFPVTPHRPTNVESCPENKAEDLW 827

QY 868 VEELMKMHTARVRDIEHLTLSLDFFRKTSRSYPEILTLKTYLHTYESEI 915
 Db 828 VEERFKAHTARVRDVELLTGDFYQEKTOQVSEILQLKTYLPTFETII 875

RESULT 4

A39216 plasma cell membrane glycoprotein PC-1 - human
 N; Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
 C; Species: Homo sapiens (man)
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
 C; Accession: A39216; S23587; S51030
 R; Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Carson, O.M.; Goding, J.W.
 J. Biol. Chem. 265, 17506-17511, 1990
 A; Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule,
 A; Reference number: A39216; MUID:9109202
 A; Accession: A39216
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-925 <BUC>
 A; Cross-references: GB:J05654
 R; Funakoshi, I.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
 Arch. Biochem. Biophys. 295, 180-187, 1992
 A; Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.
 A; Reference number: S21706; MUID:92246539
 A; Accession: S21706
 A; Status: not compared with conceptual translation
 A; Molecule type: protein
 A; Residues: 1-925 <FUN1>
 A; Cross-references: S23587
 A; Molecule type: mRNA
 A; Residues: 116-121;247-271, 'X', 273-275;279-280, 'X', 282-283;303-316;362-364;449-465;4
 A; Note: it is uncertain whether Met-1 or Met-53 is the initiator
 R; Belli, S.I.; Goding, J.W.
 Eur. J. Biochem. 226, 433-443, 1994
 A; Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph
 A; Reference number: S51030; MUID:95094801
 A; Accession: S51030
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-80 <BEL>
 C; Genetics:
 A; Gene: GDB:PDNP1; M651; NPPS
 A; Cross-references: GDB:132615; OMIM:173335
 A; Map position: 6q22-6q23
 C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology
 C; Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; t
 F; 77-97/Domain: transmembrane #status predicted

F;104-144/Domain: somatomedin B homology <SBH1>
 F;145-188/Domain: somatomedin B homology <SBH2>
 F;179,285,341,477,578,585,643,700,731,748/Binding site: carbohydrate (Asn) (covalent) # status predicted
 F;256/Binding site: AMP (Thr) (covalent) # status predicted

Query Match 39.0%; Score 1955.5; DB 1; Length 925;
 Best Local Similarity 42.2%; Pred. No. 3.5e-126;
 Matches 378; Conservative 150; Mismatches 252; Indels 115; Gaps 19;

Db 58 SCKGRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRENEA 117
 Db 107 SCKGRCFE-RTFG- -NCRCDAAVCELGNCCLDYQETCIEPEHIFTWNKFRCGEKRILTSL 163

Qy 118 CHCSEDCLARGDCCTNYQQVVKGESHWDDCEIKAECAPGFVRPPLIIIFSVDFGRAS 177
 Db 164 CACSDDDCKDKGCCINYSVCQGEKSWEEPCESINEPQCAGFETPPTLFLSLDGERAE 223

Qy 178 YMKKGSKVMPNIEKLRSQGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNNSMYDPV 237
 Db 224 YLHTNGGLLPVTISKLKKCGTYTAKNMRPVYPTKTFPNHYSTVGTGLYPESHGITDNKMYDPK 283

Qy 238 FDATFHLLRGREKFENHRWGGQPLWITATKQGVKAGTFFW-----SVV 279
 Db 284 MNASFSLSKSKEKFENPEWKGEPIWVTAKYQGLKSGTFFWPGSDVEINGIFPDIVKMYNGS 343

Qy 280 IPHERRILTIRLWLTPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSFPTAKRPK 339
 Db 344 VPFEERILAVLQLWLOLPKDERPHFTYLTLEEPDSSSGHSYGPVSSE----- 388

Qy 340 RKVAPKRRQERPVAPPKKRRRKIHMDHYAETRQDKMTNPLREIDTKTVGQLMDGILKQLK 399
 Db 389 -----
 Qy 400 LRRCVNVIFVGHDHGMDVTCRTRTEFLSNYLTVGKAGTFFW-----VIKALQRVDGMVGMLMDGLKELN 411

Db 527 RKYCG---SFHGSDNFSNMQALEVYGPVYKPKHPKEV----HP---LYQCPFTRNPRDNLGCSCNPSTLP- 582

Qy 575 PNNGTHGSLNHLRLRTNTFRPTMPEEVTRPNNPYGIMYQLQDF-----DLGCTCDDKVEPK 628
 Db 583 PNNGTHGSLNHLKKNPVPYTPKHPKEV----HP---LYQCPFTRNPRDNLGCSCNPSTLP- 634

Qy 629 NKLDELNKLRLHTKGSTEE--RH--LLYGRPAVLYR-TRYDILYHTDFESGYSEEIFMLLW 683
 Db 635 -IEDFQTQFNLTVAEEKLIKHETLPPYGRPRVQKENTICLLSQHQFMGSYQDILMPLW 692

Qy 684 TSYTVSKQAEVSSVPDHLTSCVRPDYRVSPSFQNCLAYKNDKOMSYGFLFPYPLSSSPE 743
 Db 693 TSYTVDRNDSFST--EDFSNCNLYQDFRIPSLSPVHKCSFYKNNTKVSYGFLSPQQLNKNSS 750

Qy 744 ARY-DAFLVTNMVPMYPAFKRVWNNTYQRLVKYASERNVNVISGPITFDYDGGLHDTE 802
 Db 751 GIYSEALLTTNIVPMYQSFQVIWRYFHDTLRLRKYAAERGVNVVSGPVFDYDGRCDSL 810

Qy 803 DKKIQ---YVEGSSIPVPHYYSIITSCLDFTQPADKCDGFLSVSSFILPHRPDNEESCN 859
 Db 811 ENLRQKRRVIRNQEILIPHTFFIVLTSCKDTQSPPLHCEN-LDTLAFILPHRTDNSESCV 869

Qy 860 SSEDESKWEEELMKMHTARVRDIEHTSLDFFRKTSRSYPEELTILKTYLHTYESE 914
 Db 870 HGKHDSSSWEEELMLHRAITDVEHTITGLSFYQQRKEPVSSDILKLTTHLPTFSQE 924

Qy 371 -----
 Db 371 -----

Qy 400 LRRCVNVIFVGHDHGMDVTCRTRTEFLSNYLTVGKAGTFFW-----VIKALQKVDRIVGMLMDGLKDLG 393
 Db 394 LDKCLNLILISDHDGMEQGSKCKYVYLNKLYGDVNKVYVYGAARLRPTDVPETYYSFNY 453

RESULT 5
 A27410

RESULT 8
T03293 nucleotide pyrophosphatase homolog - rice
C; Species: *Oryza sativa* (rice)
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
C; Accession: T03293
R; Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
submitted to the EMBL Data Library, April 1995
A; Description: Rice early embryogenesis gene.
A; Reference number: Z14889
A; Accession: T03293
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-479 <HSI>
A; Cross-references: EMBL:U25430; NID:9818848; PID:9818849
A; Experimental source: strain Tainung 67
C; Genetics:
A; Note: OSE4

Query Match 12.2%; Score 610; DB 2; Length 829;
Best Local Similarity 23.9%; Pred. No. 6.5e-34;
Matches 192; Conservative 127; Mismatches 278; Indels 208; Gaps 31;
QY 139 KGESEHWDDCEEIKAAEC PAGFVVRPLIIFSVGDGRAS YMKGSKVM PNIKEKLRS CGTH 198
Db 158 KARYEW--RGCC QNLGKCEL-SGYTRKPPLVILSLDGFAREY VDR--NIVQTLNHIA DCGVK 212
QY 199 SPYMRPVYPTKTEP NLYT LATGLYPESHGIVGN SMYDPV FDATEFH LRGREKFENHRWGGQ 258
Db 213 ADKVYPSYPSKTFEPNHYSTIVTGLWPESHG ITD NSVFDPTIS PVLES MKSTKY-EK FFE GE 271
QY 259 PLW-ITATKQGVKAGTFW-----SVVIPHERRILTILRWLTL PDHE 299
Db 272 PIWSVYKRKTGKKA NCFLFWGCAYNNNSGYAPDV A PAYNQELPFNRN RIDTVV EWL KLPVDE 331
Query Match 12.2%; Score 611.5; DB 2; Length 479;
Best Local Similarity 31.4%; Pred. No. 2.5e-34;
Matches 150; Conservative 65; Mismatches 132; Indels 131; Gaps 14;
Db 300 RPSVYAFYSEQP DFGH KYGPFGPEESSYGS PFTPAKRP KRQ QERPVAPP KRR 359
Db 332 RPGLITAYLHEPDNAGH-----348
QY 360 RKIHRMDH YAA ETRQDKMTNPLRE IDKIVGQLMD GLKQLKLR C RCVNVN VIFVG DGMEDVTC 419
Db 349 --YQVD-----EEDVDEKLA EIDEN LDYMSRLSEE KK LECIN FAILS DGHM QOLI-- 396
QY 420 DRTEFLSNYL TNVDDITL VPGLTRI SKFSNNA KYDPKAI IANLTCK KPDQHFKPYLKQ 479
Db 397 DKRYYFQDY L-DLKGLITA KG VV GRV--YINDTITISYNDV DFKFRCK--IDTVKTNTRS 450
QY 480 HLPK RLHYANN RIEDI HLLVER RWHV A KPLDWYKKPSGKCFQGDH GFDNKVN S M QTV 539
Db 451 DVPrTKHYSR D RYGEV--LLE----GRAGVTEYKSKAD DYE LSGD HGYD YFNPKM HTI 503
QY 540 FVGYGPTFKYKTKVPPFENI ELYN VMCD LLLG LKPA-PNNGTHGSLNHLR LNTFRPTTMPE 598
Db 504 FYARGPSFK QNTTIS PYQNTIQY MNLLGIEGA VETNGTIGFFDNIL-TNP PR RDNP T 562
QY 599 EVTRP---NY PGIMV LQSF DFLG CT CDDK VEPK NKL DELN KRLH TKGSTEER HLLY GRP 654
Db 563 NVIGECPMIA FPSV-----LKCSGNVSAETLNQ L-----SVKL TNCAFSPT 603
QY 655 AV-LYRTRYD L YHTDF ESGY SEI FIM LLLW TS YTV SKQA-----EVSSVPDH 700
Db 604 NIPLYSDNHCFQ NYCD-----NSVI YSRKG NDARRA IIEVLSR DEAS NPSN 649
QY 701 LTSC VRPD VRVSP SFPS QNC-----LAY KNDQ KOMSYGFL FPPY LS SPEAK YDA--F 749
Db 650 FTF-----LN AKY QSN C PSHI PTGSL TI RON SQ-----LSSM VDER IDV PN NF 692
QY 750 LV TNM VPMY PA FK RVNNY FQ RV K YK YAS ER NGW V NIS G P I FDY DG LHD TED KI QY V 809
Db 693 LK VLDPLQAKSMEYLN KFGK MY-----VIS GTATD IN HDG IADS-----732
QY 810 EGSSIPV PTHY SI ITSC---L DFT QPAD KCDG PLSV SSSF FILPH RPDNE ESCNS SED ES 865
Db 733 NG SVI---THI YRMLIC N STWLMN PPLC TD S DSMD TL SFI FPI TEQ STID CMSS DD-- 787
QY 866 KWVEEL MKM HTAR VRDIE HLT SL DF 890
Db 788 ----ILL DYTATI F DVER ISGFQ F 807
RESULT 9
T19494 hypothetical protein C27A7.1 - Caenorhabditis elegans
C; Species: *Caenorhabditis elegans*
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C; Accession: T19494
R; Harris, B.
submitted to the EMBL Data Library, October 1996
A; Reference number: 219132
A; Accession: T19494
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-829 <WIL>
A; Cross-references: EMBL:Z81041; PIDN:CAB02784.1; GSPDB:GN00023; CESP:C27A7.1
A; Experimental source: clone C27A7
C; Genetics:

t09933 nucleotide pyrophosphatase homolog T16L4.210 - *Arabidopsis thaliana*
C; Species: *Arabidopsis thaliana* (mouse-ear cress)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C; Accession: T09933
R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Newes, H.W.; Mayer, K.

QY	665	LYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHILTSCVRPDR-----VSPSFSON	718	QY	452	NAKYDPKAIIANLTCKKPDKQHFKPYLKQHLPKRLHYANNRRIEDIHLIVERRWHARKPL	511
Db	518	-NINCFO\$-YCE-----NSLIIHKN-----RQDVRKGVIESTFSFSRN	553	Db	142	IAKSD-----	
QY	719	CLAYKNDKQMSYGFLEPPY-----LSSSPEAKY---DAFLVTNMV	755	QY	512	DVYKKPSGCKCFQGDHGFDNKVNMSMQTIVFVGYPFTKVKPFENIELYNNVCDLLGL	571
Db	554	QSVFEN---SFSFVNTKYSIECPKLDTKDNFFTAGSEAISKLANAQKFPSMFMSKSEL	609	Db	167	E--RKYCG---GGFHGSNDNLFLNMQALEXXXXXHSTEVDSENFNEEVYNLMDLLNL	220
QY	756	PMPYPAFK-----RVWNYFQRVLWKYASERNGVNVISGPIFYDYDGHLHDTED	803	QY	572	KPAPANNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKNKL	631
Db	610	SSLSSLKDETIKFVDIWVPLS-1KTDDEYLKHGKLFVLSGLAVDRNLDGIADDE	663	Db	221	TPAFNGTH-----	
QY	632	DELNKRRLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLIWTSTVSKQ	691	QY	692	AEVSVYPDHLTSCVRPDVRSVSPSFQNCLAYKNDKQMSYGFLPFPYLSSSPEAKY-DAFL	750
RESULT	15			Db	230	-----	
A41179		protein kinase PC-1 (EC 2.7.1.-) - bovine (fragments)		QY	692	AEVSVYPDHLTSCVRPDVRSVSPSFQNCLAYKNDKQMSYGFLPFPYLSSSPEAKY-DAFL	750
N;Alternate names:	MAFP;	major acidic fibroblast growth factor-stimulated phosphoprotein		Db	230	-----	
C;Species:	Bos primigenius taurus (cattle)			QY	751	VTNMVPNYPAFKRVWNWFQQRVLVKYASERNGVNVISGPIFYDYDGHLHDTEDKIQYVE	810
C;Date:	28-May-1992	#sequence_revision 22-Apr-1995 #text_change 30-Apr-1999		Db	254	TTNIVPMYQSFQVI-----	
R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.				QY	811	GSSIIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNECSNSSEDESKWVEE	870
J. Biol. Chem. 266, 16791-16795, 1991				Db	268	-----	
A;Title:	The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein kinase			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
A;Reference number:	A41179; MUID:91358477			Db	276	LLKLIHTARITDVEHITGLSFYQQ	298
A;Accession:	A41179			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
A;Molecule type:	protein			Db	268	-----	
A;Residues:	1-26;36-56;59-67;68-133;134-144;145-267;268-300 <ODA>			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
A;Experimental source:	liver			Db	276	LLKLIHTARITDVEHITGLSFYQQ	298
R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.				QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
J. Biol. Chem. 268, 27318-27326, 1993				Db	276	LLKLIHTARITDVEHITGLSFYQQ	298
A;Title:	The major acidic fibroblast growth factor (aFGF)-stimulated phosphoprotein from esterase activities.			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
A;Reference number:	A49308; MUID:94086550			Db	268	-----	
A;Accession:	A49308			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
A;Molecule type:	protein			Db	268	-----	
A;Residues:	27-35,'X',37-58 <OD2>			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
A;Experimental source:	liver			Db	276	LLKLIHTARITDVEHITGLSFYQQ	298
A;Note:	sequence extracted from NCBI backbone (NCBIP:141583)			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
C;Superfamily:	nucleotide pyrophosphatase; somatomedin B homology			Db	276	LLKLIHTARITDVEHITGLSFYQQ	298
C;Keywords:	glycoprotein; phosphoprotein; phosphotransferase			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
F;1-25/Domain:	somatomedin B homology (fragment) <SBH>			Db	276	LLKLIHTARITDVEHITGLSFYQQ	298
F;36/Binding site:	AMP (Thr) (covalent) #status predicted			QY	871	LMKMHHTARVRDIEHLTLSLDFFRK	893
Query Match	9.1%	Score 456; DB 2; Length 300;		QY	107	RCGEVRNEENACHCSEDCLARGDCCTNYQVVCKGESEHWDDCCEEIAKAAECPAGFVRPPL	166
Best Local Similarity	18.7%	Pred. No. 6.3e-24;		Db	2	RCFE-RTFGN-CRCDAACVELGNCCLD-----	
Matches	150;	Conservative 45; Mismatches 86; Indels 522; Gaps 14;		QY	167	IIFSVDGFRASYMKKGSKYMPNIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESH	226
				Db	27	-----	
				QY	227	GIVGNSMYDPVFDATEFHLRGREKFNRWGLWTPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSP	331
				Db	53	GIIDNk-----GEPIWLT-----KSGTFFWPGSDFVKINGI	83
				QY	277	-----SVVIPHERRILTIRWLTLPLDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSP	331
				Db	84	FPDIYXVSVPFEERILALKWLQLP-----	108
				QY	332	FTPAAKRPKRKVAPKRRQERPVAPPKRRRKIHMDHYAAETRODKMTNPLREIDKIVGQL	391
				Db	109	-----	108
				QY	392	MDGILKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSFSN	451
				Db	109	-----KELNLRCLNLILLISDQGMEEQGSCKYYSF-----DSEG	141

GenCore version 4.5
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I protein - protein search, using sw model
run on: July 19, 2001, 14:44:18 ; search time 16.91 seconds
(without alignments)

title: US-09-483-831-69
perfect score: 5019
sequence: 1 MARRSSFQSCQQISLFTFAV...RSYPEILTLKTYLHTYESEI 915

scoring table: BLOSUM62

searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

maximum DB seq length: 200000000

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39;*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query :
result :

1	1955.5	39.0	873	1	PC1_HUMAN	P22413	homo sapien
2	1899.5	37.8	871	1	PC1_MOUSE	P06802	mus musculus
3	410	8.2	743	1	YCR6 YEAST	P25353	saccharomyces
4	335.5	6.7	493	1	YEB6 YEAST	P39997	saccharomyces
5	238	4.7	61	1	PPD1_BOVIN	P15396	bos taurus
6	146.5	2.9	329	1	NUC1 YEAST	P08466	saccharomyces
7	123	2.5	4655	1	LRP2_HUMAN	P98164	homo sapien
8	122	2.4	1323	1	LT23_CAEEL	P24348	caenorhabditis
9	121	2.4	1888	1	YDT2_SCHPO	Q14207	schizosaccharomyces
10	119.5	2.4	252	1	NUC1_CUNE	P81203	cunninghamiae
11	119.5	2.4	475	1	VTNC_RABIT	P22458	oryctolagus cuniculus
12	117	2.3	335	1	NUC1_SCHPO	Q10480	schizosaccharomyces
13	116.5	2.3	989	1	YD30 YEAST	P32898	saccharomyces cerevisiae
14	112	2.2	1394	1	TGFB_HUMAN	P22064	homo sapien
15	111.5	2.2	299	1	NUCG_BOVIN	P38447	bos taurus
16	111	2.2	1396	1	ITA2_DROME	P12080	drosoephila melanogaster
17	111	2.2	2871	1	FBN1_HUMAN	P35555	homo sapien
18	110.5	2.2	294	1	NUCG_MOUSE	P008600	mus musculus
19	110.5	2.2	478	1	VTNC_MOUSE	P29788	mus musculus
20	110.5	2.2	2871	1	FBN1_BOVIN	P98133	bos taurus
21	110	2.2	753	1	YJ05_CAEEL	Q01975	caenorhabditis elegans
22	109.5	2.2	1472	1	ATC9 YEAST	Q12697	saccharomyces cerevisiae
23	108.5	2.2	320	1	NUC1_SYNRA	P81204	syncephalas
24	108	2.2	1065	1	YDZ2_SCHPO	Q13710	schizosaccharomyces pombe
25	106	2.1	1106	1	STC_DROME	P40798	drosoephila melanogaster
26	106	2.1	1178	1	YN17 YEAST	P48231	saccharomyces pombe
27	106	2.1	2204	1	RRPL_NDVB	P11205	newcastle disease virus
28	106	2.1	2871	1	FBNI_MOUSE	Q61554	mus musculus
29	106	2.1	3099	1	POLG_PEMVM	Q56075	p genome protein
30	105.5	2.1	1612	1	MTDM_PARLI	Q27746	paracentrotus latus
31	105.5	2.1	1808	1	TENA_CHICK	P10039	gallus gallus
32	104.5	2.1	2201	1	TENA_HUMAN	P24821	homo sapiens
33	104.5	2.1	4289	1	TENX_HUMAN	P22105	homo sapiens

34	104	BFR1_YEAST	1	P38934	saccharomyces
35	104	AMIA_STRPN	1	P18791	streptococcus
36	104	KPC2_DROME	1	P13677	drosophila
37	104	DPOM_NEUTIN	1	P33538	neurospora
38	103.5	NUCG_HUMAN	1	Q14249	homo sapien
39	103	P100_HSV7J	1	P52519	human herpes
40	103	BAR3_CHITE	1	Q03376	chironomus
41	102.5	PP11_HUMAN	1	P21128	homo sapien
42	102.5	FHUA_ECOLI	1	P06971	escherichia
43	102.5	EGFR_DROME	1	P04412	drosophila
44	102	IDS_MOUSE	1	Q08890	mus musculus
45	102	FNBA_STAAU	1	P14738	staphylococcus

ALIGNMENT S

RESULT 1
PC1_HUMAN
ID PC1_HUMAN
STANDARD; PRT;
873 AA.
D23413; CONCEN;
CONCEN

01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE (EC 3.6.1.9) (NPPASE)].
PDNP1 OR PC1 OR NPPS.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=91009202; PubMed=2211644;
Buckley M.F., Loveland K.A., McKinstry W.J., Garson O.M., Goding J.W.; "Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule, amino acid sequence, and chromosomal location." ; J. Biol. Chem. 265:17506-17511(1990).

RP SEQUENCE FROM N.A.
 RX MEDLINE=92246539; PubMed=1315502;
 RA Funakoshi I., Kato H., Horie K., Yano T., Hori Y., Kobayashi H.,
 Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,
 Yamashina I.;
 RT "Molecular cloning of cDNAs for human fibroblast nucleotide
 pyrophosphatase.";
 RT Arch. Biochem. Biophys. 295:180-187(1992).
 [3]
 RN RP SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.
 RX MEDLINE=99408501; PubMed=10480624;
 RA Pizzutti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,
 RA Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,
 RA Tassi V., Trischitta V.;
 RT "A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding
 region is strongly associated with insulin resistance.";
 RT Diabetes 48:1881-1884(1999).
 -!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
 -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 OLIGO-NUCLEOTIDES.
 -!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
 -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 -!- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
 OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
 OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.
 -!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.

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 CC use by non-profit institutions.

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QY	515	KKPSGKCFQQGFDNKVNNSMQTVFVGYGPTEKYKTKVPPFENIELYNVMC DLLGLKPA	574
Db	475	RKYCG --- SGFHGSNDNFSSNMQALFVGYPGPGEKHGIEADTFENIEVYNLMDLLNLTPA	530
QY	575	PNNGTHGSLNHLRTNTFRPTMPEEVTRPNYPGIMYLQSDF --- DLGCTCDDKVEPK	628
Db	531	PNNGTHGSLNHLKNPVYTPKHPKEV --- HP --- LVQCPFTRNPRDNLGCSCNPSILP-	582
QY	629	NKLDELNKRLLHTKGSTEE -- RH -- LLYGRPAVLYR - TRYDILYHTDFESGYSEIFLMLLW	683
Db	583	- IEDFQTQFNLTVAEEKIIKHETLPPYGRPRVLQKENTICLLSQHQMSGYSQDILMPLW	640
QY	684	TSYTISKQAEVSSVPDHLTSCVRPDVRVSFSQNCLAYKNDKQMSYGFLFPYPLSSSPE	743
Db	641	TSYTVDRNDSFST -- EDFSNCLYQDFRIPLSPVHKCSFYKNNTKSYGFLSPPQLNKNS	698
QY	744	AKY -DAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPIFDYDYDGJLHDTE	802
Db	699	GIYSEALLTTNTIVPMYQSFQVITWRYFHDTLLRKYAAERNGVNVSQPVFDDYDGRCDSL	758
QY	803	DKIKQ --- YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCN	859
Db	759	ENLRQKRRVIRNQEILLIPHTEFFIVLTSCKDTSPHLHCEN - LDTLAFILPHRTDNSESCV	817
QY	860	SSEDESKWVEELMKMHTARVRDIEHLSLDFFRKTSRSYPEILTLLKTYLHTYESE	914
Db	818	HGKHDSSSWVEELLMLHRARITDVEHITGLSFYQQRKEPVSDILKLKTHLPTFSQE	872
RESULT 2			
PC1_MOUSE			
ID	PC1_MOUSE	STANDARD;	PRT;
AC	P06802;		871 AA.
DT	01-JAN-1998 (Rel. 06, Created)		
DT	01-AUG-1991 (Rel. 19, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE (EC 3.6.1.9) (NPPASE)].		
DE	PDNP1 OR PC1 OR NPPS.		
GN	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxID=10090;		
RN	[1]	SEQUENCE FROM N.A.	
RX	MEDLINE=87165906; PubMed=3104326;		
RA	van Driel T.R., Goding J.W.;		
RT	"Plasma cell membrane glycoprotein PC-1. Primary structure deduced from cDNA clones."		
RL	J. Biol. Chem. 262:4882-4887(1987).		
RN	[2]	PARTIAL SEQUENCE.	
RX	MEDLINE=85056299; PubMed=3917281;		
RA	Stearne P.A., van Driel T.R., Grego B., Simpson R.J., Goding J.W.;		
RT	"The murine plasma cell antigen PC-1: purification and partial amino acid sequence."		
RT	J. Immunol. 134:443-448(1985).		
RN	[3]	FUNCTION, AND SEQUENCE FROM N.A.	
RX	MEDLINE=91271356; PubMed=1647027;		
RA	Rebbe N.F., Tong B.D., Finley E.M., Hickman S.;		
RT	"Identification of nucleotide pyrophosphatase/alkaline phosphodiesterase I activity associated with the mouse plasma cell differentiation antigen PC-1."		
RT	Proc. Natl. Acad. Sci. U.S.A. 88:5192-5196(1991).		
RN	[4]	SEQUENCE OF 169-185 FROM N.A.	
RX	MEDLINE=86094275; PubMed=3001713;		
RA	van Driel T.R., Wilks A.F., Pietersz G.A., Goding J.W.;		
RT	"Murine plasma cell membrane antigen PC-1: molecular cloning of cDNA and analysis of expression."		

Proc. Natl. Acad. Sci. U.S.A. 82:8619-8623 (1985).
 -1- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.

-1- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.

-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.

-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF ANTI BODY-SECRETING CELLS.

-1- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.

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EMBL; J02700; AAA39893.1; ALT_INIT.

DR EMBL; M12552; AAA39892.1; -.

DR PIR; A27410; A27410.

DR MGI; 97370; Pdnpl.

DR InterPro; IPR001212; -.

DR InterPro; IPR002591; -.

DR Pfam; PF01663; Phosphodiester; 1;

DR Pfam; PF01033; Somatomedin_B; 2.

DR PROSITE; PS00524; SOMATOMEDIN_B; 2.

KW Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase.

FT MOD_RES P1 BLOCKED.

FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DOMAIN 46 871 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.

FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.

FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 871 AA; 99487 MW; 80848FB81071F70AA CRC64;

RESULT 3 YCR6_YEAST STANDARD; PRT; 743 AA.

ID P2353; AC P2353; DT 01-MAY-1992 (Rel. 22, Created)

DE HYPOTHETICAL 84.9 KDA PROTEIN IN PMP1-FEN2 INTERGENIC REGION.

GN YCR026C OR YCR246.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Fungi; Ascomycota; Saccharomyces cerevisiae; Saccharomyces.

NCBI_TaxID=4932; RN [1]

SEQUENCE OF 1-244 FROM N.A.

RP Pohl F., Richterich P., Wurst H.; RA Submitted (MAR-1992) to the EMBL/GenBank/DDJB databases.

RN [2]

RP SEQUENCE OF 244-743 FROM N.A.

RX MEDLINE=92245758; PubMed=1574926;

RA Bolle P.-A., Gilliquet V., Berben G., Dumont J., Hilger F.;

RT "The complete sequence of K3B, a 7.9 kb fragment between PGK1 and

CRY1 on chromosome III, reveals the presence of seven open reading

frames.";

RT Year 8:205-213 (1992).

CC -1- SIMILARITY: TO YEAST YEL016C.

CC

DR	EMBL; X59720; CAA42318.1; -.	RA	Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
DR	PIR; S19437; S19437.	RA	
DR	S27380; S27380.	RL	Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
DR	SGD; SGD000621; YCR026C.	CC	-1 - SIMILARITY: TO YEAST YCR26C.
DR	InterPro; IPR002591; -.	CC	
DR	PFam; PF01663; Phosphodiest; 1.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
KW	Hypothetical protein; Transmembrane.	CC	
FT	TRANSMEM 114 135 POTENTIAL.	CC	
SEQUENCE	743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;	CC	
Query Match	8.28; Score 410; DB 1; Length 743;	Query Match	6.7%; Score 335.5; DB 1; Length 493;
Best Local Similarity	24.0%; Pred. No. 5.4e-22;	Best Local Similarity	24.8%; Pred. No. 7.6e-17;
Matches	126; Conservative 76; Mismatches 178; Indels 146; Gaps 18;	Matches	116; Conservative 71; Mismatches 153; Indels 127; Gaps 21;
QY	164 PPLIIFSDGFRASYM-KKGSKVMPNIEKLRSRG----THSPYMRPVYPTKTFPNLYTLA 218	QY	167 IIFSVDGFRASYM-KKGSKVMPNIEKLRSRG----THSPYMRPVYPTKTFPNLYTLATGL 221
Db	168 PLTIVISLDGFHPSLISKRNTPFLHDLYELKYDGGMNITSTPMPSPPTETFPNHWTLLV 227	Db	79 ILLISDGFHPRLLDAKYTPFLYNLHNLRSPTYDMNITTAPYMPIPSFTPTQFPNHWSMVTGK 138
QY	219 TGLYPESHGIVGNSMYDPVFDATEFHLLRGREKFHNHRWGG---QPLWITATKQ----GVK 270	Db	222 YPESHIGIVGNSMYDPVFDATEFHLLRGREKFHNHRWGG---GQPLW--ITATKQG-VKAGTFFW 276
Db	228 TGQWPIHHGIVSNVFWDPDLNEEFH---PGVLDPRIWNNDTEPIWQTVQSAFDGDIPFK 284	Db	139 YPTEHIGIVSNIFWDNFTSSEFR--PNNLDARIWNSNTADPIWQLQTESQEYKVATHMW 195
QY	271 AGTFFW-----	QY	277 ---SWV-----IPHER---
Db	285 AATHMWPGSDVNNTKYKTEEKLOPEHKKPPIARERTPFYFDEFNAKEPLSQKLSKITEYVD 344	Db	196 PGSEVYYEDHGDVPRERMFYFGKFNQWEKLQDKLAQIFRYIDMPQLKDRPELVSYIPN 255
QY	295 LPD-HERPSVYAFYSEQOPDSGHKYGPGFGEESYGSPPFTPAKPKRKVAKPQRQERPVA 353	QY	311 PDFSGHKYGPFGPEESSYGSPPFTPAKPKRKVAPKRQERPVAA 310
Db	345 MSTLNERPQLLIGYVPNVDAFGHKHG--YPSSEY-----	Db	371 ETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHG 413
QY	354 PPKKRRRK1IHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHG 413	Db	266 DLRKRLQKLIGEVGDFFLDLIEGLQKRNLLKISNVMIVSDHGMNSNVNANDGEHVVWER 325
Db	378 -----YY-----EDFTETLGEVDTFLKOLVESLQERNLTSFTNLVIVSDHGV 418	QY	377 -----LSNYLTNVDDITLVPGLRGRISKSFSNNAKYDPKA 459
QY	414 MEDWTCD-----RTEFLSNLYLTNVDDITLVPGLRGRISKSFSNNAKYDPKA 511	Db	256 VDSYGHHSFG-----
Db	419 MSDIVVPSNVIIWEDLDEKLRKDYVSH-----AYLEGPMMAISLKDGSNI----NE 466	QY	378 -----RTEFLSNLYLTNVDDITLVPGLRGRISKSFSNNAKYDPKA 459
QY	460 IIANLJTKKKPDQHFKPYLKQHLPKRLHY--ANNRRIEDIHLLVERRWHYARKPL-----	Db	379 ETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEF----424
Db	467 VYHNLKTSIDEKDKYTVYNGNFPKEWNFNDGKNHHMASIWVPEPGYAVMKKEQLKKVAK 526	QY	380 -----LSNYLTNVDDITLVPGLRGRISKSFSNNAKYDPKA 459
QY	512 -DVYKKPSGKCFQQGDHFDNKVNMSMQTVFVGYGPTFKYKTKVPPFENIENYVMCDLLG 570	Db	381 ILKEDFDPSWKYFQYDNRKHRYDDRVGDIWILADEVYAIVKEMGDV---PIG---IMGTH 435
Db	527 GHDKDKNEDNVFTIGSHGVDNNAIDMRSVFIGMGPYFP-QGYIEPFQNTIEYNLLCDICG 585	QY	382 VFPADAMSAFISHLYN---EGPMMMVCLKNPDRKQWICDLIAQUEKAYGDEISRKFHV 381
QY	571 LKPAAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFD 616	Db	383 YLKOHLPP---KRLHYANNR----RIEDIHLLVERRWHYARKPLDVYKKPSGKCFQQGDH 527
Db	586 VAERDRNSNDGT--GMLMNQLREPQSSEEVE-----IEDDFD 620	QY	384 -----YKQHLP---KRLHYANNR----RIEDIHLLVERRWHYARKPLDVYKKPSGKCFQQGDH 527
RESULT	4	RESULT	5
ID	YEB6_YEAST STANDARD; PRT; 493 AA.	PPD1_BOVIN ID	PPD1_BOVIN STANDARD; PRT; 61 AA.
AC	P39997; 31, Created)	AC	P15396; 14, Created)
DT	01-FEB-1995 (Rel. 31, Last sequence update)	DT	01-APR-1990 (Rel. 14, Last sequence update)
DT	01-FEB-1995 (Rel. 31, Last annotation update)	DT	01-APR-1990 (Rel. 14, Last annotation update)
GN	YEL016C. HYPOTHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION.	DT	01-FEB-1994 (Rel. 28, Last annotation update)
OS	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomyctaceae; Saccharomyces cerevisiae (Baker's yeast).	DE	PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOSPHODIESTERASE) (FRAGMENT).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyctaceae; Saccharomyces cerevisiae (Baker's yeast).	DE	Bos taurus (Bovine).
OC	Saccharomyctales; Saccharomyctaceae; Saccharomyces.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovoidea; Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=4932; [1]	OC	NCBI_TaxID=9913; [1]
RN	SEQUENCE FROM N.A.	OX	
RP	STRAIN=S288C / AB972;	RN	
RC	Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Moesdale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,	RA	

RP SEQUENCE; TISSUE=Intestine;
 RC MEDLINE=8523451; PubMed=2989287;
 RX Culp J.S., Blytt H.J., Hermodson M., Butler L.G.;
 RA "Amino acid sequence of the active site peptide of bovine intestinal
 RT 5'-nucleotide phosphodiesterase and identification of the active
 site residue as threonine.";
 RT J. Biol. Chem. 260:8320-8324 (1985).
 -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 CC PIR; A25274; A25274.
 DR KW Hydrolase.
 FT NON_TER 1 39 FORMS A PHOSPHOTHREONINE INTERMEDIATE.
 ACT_SITE 61 AA; 6999 MW; 580C8B4807A61C84 CRC64;
 SQ SEQUENCE

Query Match 6
 Best Local Similarity 4.78; Score 238; DB 1; Length 61;
 Matches 40;保守性 66.7%; Pred. No. 5.4e-11;
 AC NUC1_YEAST STANDARD; PRT; 329 AA.
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MITOCHONDRIAL NUCLEASE (EC 3.1.30.-).
 GN NUC1 OR YJL208C OR J0310 OR HRE329.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomyces.
 OC Nucleic Acids Res. ID=4932;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=2935-106;
 RX MEDLINE=88233924; PubMed=2836792;
 RA Vincent R.D., Hofmann T.J., Zassenhaus H.P.;
 RT "Sequence and expression of NUC1, the gene encoding the mitochondrial
 nuclelease in *Saccharomyces cerevisiae*."
 RT Nucleic Acids Res. 16:3297-3312(1988).
 RN [2] SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=95274326; PubMed=7754713;
 RA Purnelle B., Coster F., Goffeau A.;
 RT "The sequence of a 36 kb segment on the left arm of yeast chromosome
 X identifies 24 open reading frames including NUC1, PRP21 (SPP91),
 CDC6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1
 and two homologues to chromosome III genes."
 RL Yeast 10:1235-1249(1994).
 RN [3] SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=95242842; PubMed=7725802;
 RA Vandebroek M., Durand P., Bolle P.-A., Dion C., Portetelle D.,
 RA Hilger F.;
 RT "Sequence analysis of a 40.2 kb DNA fragment located near the left
 telomere of yeast chromosome X."
 RL Yeast 10:1657-1662(1994).
 RN [4] SEQUENCE OF 204-329 FROM N.A.
 RX MEDLINE=90014786; PubMed=2552292;
 RA Liu Y., Dieckmann C.L.;
 RT "Overproduction of yeast viruslike particles by strains deficient in
 a mitochondrial nuclease."
 RT

RL Mol. Cell. Biol. 9:3323-3331(1989).
 CC -!- FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY.
 CC -!- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
 CC -!- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
 CC FAMILY.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; X06670; CAA29870_1;
 DR EMBL; X77688; CAA54748_1;
 DR EMBL; 234098; CAA84003_1;
 DR EMBL; 249483; CAA89505_1;
 DR EMBL; M28067; AAA34457_1;
 DR PIR; S05888; NCBYN1.
 DR PIR; S46621; S46621.
 DR HSSP; P13717; 1SMN.
 DR SGD; S0003744; NUC1.
 DR InterPro; IPR001604;
 DR Pfam; PF01223; Endonuclease_1.
 DR PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Magnesium; Mitochondrion;
 KW Inner membrane.
 FT ACT_SITE 138 AA; 37209 MW; CAEC967BCB00943C CRC64;
 SQ SEQUENCE

Query Match 565 MCDLLGLKPAPNNGTHGSILNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDK 624
 Best Local Similarity 2.98; Score 146.5; DB 1; Length 329;
 Matches 79; Conservative 48; Mismatches 159; Indels 61; Gaps 16;

QY	VEPKNKLDLNKRLHHTKGSTEERHLIYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWT 684	Db	1 MCSRILLSGLGLGAGTGTLTYLL-LNKHSP---QIETPYP-----
QY	SYTVSKQAEVSSVPDHLTSVCPDVRVSPSPFSOINCLAYKNDQMSYGFLFPPY-LSSSPE 743	Db	39 --PTQKPNs-NIQSHSFNWDPSGFFKYGFPGPi --- HDLQNREEFISCSYNRQTNQPYW 91
QY	92 LEHITPESLAARNADRKNSTFFKEDEVIPKEFKRGKLDRYFR-SGYDRGHQAPAADAKFSQQ 150	Db	92 LEHITPESLAARNADRKNSTFFKEDEVIPKEFKRGKLDRYFR-SGYDRGHQAPAADAKFSQQ 150
QY	744 AKYDAFLVTNMVPMY-PAFKR-VW-- NYFQRVLVKKYASERNGVNISGPFDYDYDGL 798	Db	151 AMDDTFYLNSNCMPQVGEGENRDYWAHLEYFCRGTLKYKS---VRIVTGPLYLPKKDPI 206
QY	799 HDTEDKIKQYVEGS--SIVPVTHYSSIIITSCLDFTQPADKCDGPLSVSSFILPHRP-DNE 855	Db	207 -DNKFRVNYEVIGNPPSIAVPTHEFFKLIVAEAPPNTANPARE---DIAVAFAVLPNEPISNE 262
QY	856 ESCNSSEDSEKWWEEELMKMHTARVDRDIEHTLSLDFFRKTSTSYPEIL 902	Db	263 TKLTDFE-----VPTDALESTERSTGLLELLQKVPPSKKKAL 295

RESULT 7
 ID LRP2_HUMAN STANDARD; PRT; 4655 AA.
 AC P98164; Q00711; Q16215;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
 DE (GLYCOPROTEIN 330).
 GN LRP2.

OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1] RP SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RX	Medline=96305376; PubMed=8706697;
RA	Hjaelm G., Murray E., Crumley G., Harazim W., Lundgren S., Onyango I., Ek B., Larsson M., Juhlin C., Hellman P., Davis H., Akerstroem G., Rask L., Morse B.;
RA	"Cloning and sequencing of human gp330, a Ca(2+)-binding receptor with potential intracellular signaling properties." Eur. J. Biochem. 239:132-137(1996).
RN	[2] RP SEQUENCE OF 2705-4453 FROM N.A.
RC	Knaak C., Argraves W.S.;
RX	Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
RN	[3] RP SEQUENCE OF 3833-4453 FROM N.A.
RC	TISSUE=Kidney;
RX	Medline=95048397; PubMed=7959795;
RA	Korenberg J.R., Argraves K.M., Chen X.N., Tran H., Strickland D.K., Argraves W.S.;
RA	"Chromosomal localization of human genes for the LDL receptor family member glycoprotein 330 (LRP2) and its associated protein RAP (LRPAP1)." Genomics 22:88-93(1994).
RN	[4] RP SEQUENCE OF 4139-4406 FROM N.A.
RX	Medline=94244704; PubMed=8187828;
RA	Lundgren S., Hjelm G., Hellman P., Ek B., Juhlin C., Rastad J., Klareksog L., Aakerstrom G., Rask L.;
RA	"A protein involved in calcium sensing of the human parathyroid and placental cytotrophoblast cells belongs to the LDL-receptor protein superfamily." J. Biol. Chem. 270:13070-13075(1995).
RT	"Identificaton of glycoprotein 330 as an endocytic receptor for apolipoprotein J/clusterin." J. Biol. Chem. 270:13070-13075(1995).
RT	"FUNCTION: BINDS SPECIFICALLY CLUSTERIN WITH HIGH AFFINITY, BUT ALSO LIGANDS IN COMMON WITH OTHER FAMILY MEMBERS: PLASMINOGEN, EXTRACELLULAR MATRIX COMPONENTS, PLASMINOGEN ACTIVATOR-PLASMINOGEN ACTIVATOR INHIBITOR TYPE I COMPLEX, APOLIPOPROTEIN E-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE, LACTOFERRIN AND CALCIUM."
CC	-!- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS APROTININ, AMINOGLYCOSIDES AND POLYMYXIN B (BY SIMILARITY).
CC	-!- FUNCTION: MAY PARTICIPATE IN REGULATION OF PARATHYROID-HORMONE AND PARA-THYROID-HORMONE-RELATED PROTEIN RELEASE.
CC	-!- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-ASSOCIATED PROTEIN (RAP).
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-!- TISSUE SPECIFICITY: ABSORPTIVE EPITHELIUM, INCLUDING RENAL PROXIMAL TUBULES.
CC	-!- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.
CC	-!- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
CC	-!- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
CC	-!- SIMILARITY: CONTAINS 4 SH3-BINDING DOMAINS.
CC	-!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	or send an email to license@isb-sib.ch.)
CC	EMBL; U33837; AAB41649.1;
DR	DR InterPro; IPR000033;
DR	DR InterPro; IPR000152;
DR	DR InterPro; IPR000561;
DR	DR InterPro; IPR001881;
DR	DR InterPro; IPR002172;
PFam	PF00008; EGF; 13.
PFam	PF00057; LDL_recept_a; 36.
PFam	PF00058; LDL_recept_b; 37.
PRINTS	PRINTS; PR00261; LDLRECEPTOR.
ASX_HYDROXYL	ASX_HYDROXYL; 4.
PROSITE	PS00010; ASX_HYDROXYL;
PROSITE	PS00022; EGF_1; 1.
PROSITE	PS01186; EGF_2; 9.
PROSITE	PS01187; EGF_CA; 3.
PROSITE	PS01209; LDLRA_1; 31.
PROSITE	PS50068; LDLRA_2; 36.
KW	Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane; Receptor; EGF-like domain; Signal; Polymorphism.
KW	KW SIGNAL 1 25
FT	FT CHAIN 26 4655
FT	FT DOMAIN 26 4423
FT	FT TRANSMEM 4424 4446
FT	FT DOMAIN 4447 4655
FT	FT DOMAIN 26 64
FT	FT DOMAIN 65 105
FT	FT DOMAIN 106 144
FT	FT DOMAIN 145 181
FT	FT DOMAIN 182 219
FT	FT DOMAIN 220 258
FT	FT DOMAIN 264 308
FT	FT DOMAIN 309 347
FT	FT DOMAIN 348 386
FT	FT DOMAIN 436 477
FT	FT DOMAIN 479 520
FT	FT DOMAIN 522 567
FT	FT DOMAIN 569 612
FT	FT DOMAIN 613 653
FT	FT DOMAIN 659 705
FT	FT DOMAIN 753 794
FT	FT DOMAIN 796 836
FT	FT DOMAIN 838 880
FT	FT DOMAIN 882 924
FT	FT DOMAIN 970 1014
FT	FT DOMAIN 1024 1062
FT	FT DOMAIN 1065 1103
FT	FT DOMAIN 1107 1145
FT	FT DOMAIN 1147 1185
FT	FT DOMAIN 1186 1224
FT	FT DOMAIN 1228 1268
FT	FT DOMAIN 1269 1307
FT	FT DOMAIN 1310 1350
FT	FT DOMAIN 1349 1389
FT	FT DOMAIN 1390 1429
FT	FT DOMAIN 1478 1519
FT	FT DOMAIN 1521 1562
FT	FT DOMAIN 1566 1608
FT	FT DOMAIN 1610 1653
FT	FT DOMAIN 1655 1695
FT	FT DOMAIN 1700 1741
FT	FT DOMAIN 1790 1831
FT	FT DOMAIN 1833 1881
FT	FT DOMAIN 1883 1929
FT	FT DOMAIN 1931 1971
FT	FT DOMAIN 1972 2012
FT	FT DOMAIN 2018 2059
FT	FT DOMAIN 2107 2155
FT	FT DOMAIN 2157 2200

FT DOMAIN	2202	2244	LDL-RECEPTOR CLASS B	22.	Db	1456 HNTYSLVENGSYIVAVDFDSISGRIFWSDATQGKTWSAFQNGTDRRVVFDSSTIILTETIA	1515
FT DOMAIN	2246	2288	LDL-RECEPTOR CLASS	B 23.	QY	246 ---GREKF--	
FT DOMAIN	2290	2331	LDL-RECEPTOR CLASS	B 24.		NR-----	
FT DOMAIN	2342	2383	EGF-LIKE 9.			W-WGG 257	
FT DOMAIN	2431	2476	LDL-RECEPTOR CLASS	B 25.		:	
FT DOMAIN	2478	2517	LDL-RECEPTOR CLASS	B 26.	Db	1516 IDWGRNLYWTDXALETIEVSKIDGSHRTVLISKNLTNPQLALDPRMNEHLLFWSDWGH	1575
FT DOMAIN	2519	2561	LDL-RECEPTOR CLASS	B 27.	QY	258 QPLWITATKQG---VKAGTFFW- SVVIPHERRLTILRWLTLPDHERPSVYAFYSEQ	310
FT DOMAIN	2563	2603	LDL-RECEPTOR CLASS	B 28.		1 : : :	
FT DOMAIN	2604	2646	LDL-RECEPTOR CLASS	B 29.	Db	1576 HPRIERASMDGSMRTVIVQDKIFWPCGLTIDPNRRLYFM-----DSYLDYMDF	1624
FT DOMAIN	2651	2693	EGF-LIKE 10.		QY	311 PDFSGHKYGPFGPEESSYGSPPTPAKRPKRKVAPKRRQ-----	
FT DOMAIN	2698	2738	LDL-RECEPTOR CLASS	A 16.		ERPV A 353	
FT DOMAIN	2739	2777	LDL-RECEPTOR CLASS	A 17.		:	
FT DOMAIN	2778	2819	LDL-RECEPTOR CLASS	A 18.		--HRRQVIASDLIIRHPYALTLEEDSVY	1656
FT DOMAIN	2820	2861	LDL-RECEPTOR CLASS	A 19.			
FT DOMAIN	2862	2901	LDL-RECEPTOR CLASS	A 20.	QY	354 PPKKRRRKIHMDHYAAETRODKMTN--PLREIDKIVGQLMGDGLKQLKLRCVNIVFG	410
FT DOMAIN	2904	2945	LDL-RECEPTOR CLASS	A 21.		4 : : : :	
FT DOMAIN	2946	2990	LDL-RECEPTOR CLASS	A 22.	Db	1657 WTDRACTRVMRANKWHGGNOSVVMYNIQWPLGIVAVHPSKQPNNSVNPCAFCSRCSHLCLLS	1716
FT DOMAIN	2991	3029	LDL-RECEPTOR CLASS	A 23.	QY	411 DHGMEDVTC-----	
FT DOMAIN	3030	3070	LDL-RECEPTOR CLASS	A 24.		425	
FT DOMAIN	3073	3110	LDL-RECEPTOR CLASS	A 25.			
FT DOMAIN	3111	3151	EGF-LIKE 11.				
FT DOMAIN	3152	3192	EGF-LIKE 12. CALCIUM-BINDING (POTENTIAL).				
FT DOMAIN	3239	3280	LDL-RECEPTOR CLASS	B 30.	QY	426 -----SNYLTNVDDITLVPGTLAGRIRSKFSNNNAKYDPKAIIANLTCKKPDKQHF	473
FT DOMAIN	3282	3331	LDL-RECEPTOR CLASS	B 31.		4 : : : :	
FT DOMAIN	3333	3375	LDL-RECEPTOR CLASS	B 32.	Db	1777 IQNGLDVEFDDEAQYIYWEN----PGEIHRVKTDTGN-----RTVFA SISMYGPMSML	1826
FT DOMAIN	3377	3418	LDL-RECEPTOR CLASS	B 33.	QY	474 K-PYLROHLPKRLHYANNRRIEDIHLV----ERRWHVARK-----	
FT DOMAIN	3419	3459	LDL-RECEPTOR CLASS	B 34.		-----PLDVYKKPS 518	
FT DOMAIN	3465	3509	EGF-LIKE 13.				
FT DOMAIN	3510	3550	LDL-RECEPTOR CLASS	A 26.	Db	1827 ALDWISRN L-----YSTNPRTQSIEVLT LHGDIRYRKTLI ANDGTALGVGFPI GITVDPA	1881
FT DOMAIN	3551	3591	LDL-RECEPTOR CLASS	A 27.	QY	519 GKCFQGDHGF DNKV-----NSMQTVFVG YGPTFKYKT KVPFENIELYNYMCD	567
FT DOMAIN	3592	3632	LDL-RECEPTOR CLASS	A 28.		567	
FT DOMAIN	3633	3673	LDL-RECEPTOR CLASS	A 29.	Db	1882 RGKLYWSDQGTDSGPVAKIASANMDGTSVKTFLFTG-----	
FT DOMAIN	3676	3716	LDL-RECEPTOR CLASS	A 30.	QY	568 LLGLKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPG-----IMYLOQSDFDLGC TCD	623
FT DOMAIN	3717	3756	LDL-RECEPTOR CLASS	A 31.		623	
FT DOMAIN	3757	3795	LDL-RECEPTOR CLASS	A 32.	Db	1925 TLDIEE-----QKLYWAVTGRGV----IERGNVDGTDRMILVHQ LSHPWGIAVHD	1970
FT DOMAIN	3796	3834	LDL-RECEPTOR CLASS	A 33.	QY	624 KVEPKNKLDELNKRLHTKGSTEERHLLYGRPAVLYRT--RYDILYHTDFESGYSE FEF L--	679
FT DOMAIN	3840	3880	LDL-RECEPTOR CLASS	A 34.		679	
FT DOMAIN	3881	3922	LDL-RECEPTOR CLASS	A 35.	Db	1971 -----SFLYYTDEQYE VIERVDKATGANKIVL RD 1999	
FT DOMAIN	3926	3964	LDL-RECEPTOR CLASS	A 36.	QY	680 -----MLLWTSYTVSKQAEVSS-----	
FT DOMAIN	3966	4006	EGF-LIKE 14.			680	
FT DOMAIN	4007	4048	EGF-LIKE 15. CALCIUM-BINDING (POTENTIAL).				
FT DOMAIN	4154	4195	LDL-RECEPTOR CLASS	B 35.	Db	2000 NVPNLRGLQVYHRRNAAESNGCSNNMMACQQICL PVP GGLEFS CA-----	
FT DOMAIN	4197	4239	LDL-RECEPTOR CLASS	B 36.	QY	721 AYKN DKQMSYGF-LFP PYLSSPEAKYDAFLY TNMVP MYP AFA KRVW NYFQRV L VKYASE	779
FT DOMAIN	4242	4282	LDL-RECEPTOR CLASS	B 37.		779	
FT DOMAIN	4330	4368	EGF-LIKE 16.		Db	2045 -----CATGFKLNP DPN SCS C-----CYSPIV VSMSL SAIRGFS LE LSDHS ESETM VPVAGQG	2094
FT DOMAIN	4377	4411	EGF-LIKE 17.		QY	780 RNG----VNVISGPIFDYD DGLH DTE D KIQY-VEGSSI -PV PTH	819
					Db	2095 RNALHV DV DSSGFIYWCDESSV ASDNAIRRIKP DGSS LMMNIVTH	2140
					RESULT 8		
					LT23_CAEEL		
					ID LT23_CAEEL	STANDARD;	PRT; 1323 AA.
					AC P24348;		
					DT 01-MAR-1992 (Rel. 21, Created)		
					DT 01-MAR-1992 (Rel. 21, Last sequence update)		
					DT 01-OCT-2000 (Rel. 40, Last annotation update)		
					DE LET-23 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112).		
					GN LET-23 OR KIN-7 OR ZK1067.1.		
					OS Caenorhabditis elegans.		
					OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae; Rhabditidae; Peleoderaiae; Caenorhabditis.		
					OC NCBI_TaxID=6239;		
					RN [1]		
					RP SEQUENCE FROM N.A.		
					RX MEDLINE=91080919; PubMed=1979659;		
					RA Aronian R.V., Koga M., Mendel J.E., Ohshima Y., Sternberg P.W.;		
					"The let-23 gene necessary for Caenorhabditis elegans vulval		

RT Induction encodes a tyrosine kinase of the EGF receptor subfamily. ";

RL Nature 348:693-699(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=9617760; PubMed=8604137;

RA Sakai T., Koga M., Ohshima Y.;

RT "Genomic structure and 5' regulatory regions of the let-23 gene in the nematode *C. elegans*.";

RL J. Mol. Biol. 256:548-555(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Thomas K.;

RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP MEDLINE=94147981; PubMed=8313880;

RA Aroian R.V., Les G.M., Sternberg P.W.;

RT "Mutations in the Caenorhabditis elegans let-23 EGFR-like gene define elements important for cell-type specificity and function.";

RL EMBO J. 13:360-366(1994).

CC -!- FUNCTION: TYROSINE KINASE RECEPTOR REQUIRED FOR THE INDUCTION OF C.ELEGANS VULVA. POSSIBLE RECEPTOR FOR THE INDUCTIVE SIGNAL REQUIRED FOR VULVAL DEVELOPMENT. ACTIVATED BY LIN-3 AND ACTS BY WAY OF LET-60 RAS. THE LIN-3/LET-23 PAIR IS A SIMPLIFIED VERSION OF THE MAMMALIAN NEUREGULIN-ERBB NETWORK.

CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC

DR X71767; CAA40919.1; ALT_SEQ.

DR EMBL; D63426; BAA09729.1; ALT_INIT.

DR EMBL; 270038; CAA93882.1; -.

DR PIR; S13422; S13422.

DR HSSP; P11362; 1FGI.

DR WormPep; ZK1067.1; CE03840.

DR InterPro; IPR000494; -.

DR InterPro; IPR000719; -.

DR Pfam; PF00757; Furin-like; 1.

DR Pfam; PF01030; Recop_L_domain; 2..

DR Pfam; PF00069; Pkinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Tyrosine-protein kinase; ATP-binding; phosphorylation;

KW Transmembrane; Glycoprotein; Receptor; Signal.

FT SIGNAL 1 22

FT DOMAIN 842 1323

FT DOMAIN 885 1152

FT TRANSMEM 819 841

FT DOMAIN 842 1323

FT DOMAIN 885 1323

FT NP_BIND 891 899

FT BINDING 919 919

FT ACT_SITE 1010 1010

	Query Match	Match	Score	Length
Best Local Matches	Local Similarity	18.4%	2.4%	1323;
Matches	Conservative	106;	Pred. No.	0.73;
	Mismatches	290;	Indels	264;
	Gaps	43;		
Qy 48	SDSPWTNISGSCK-	-----	-GRCEELQEAGPPDCRCDNL-----	-KSYTSSCC 87
Db 225	NDKCGWGSDDNCQRVYRSVCPKSQCFYSNSTSSYEC-CDSACLGGCTGHGPKNCTACS	283		
Qy 88	HDFDELCLXTARGWECKDRCGEV-----	-RNEENACHCSEDC-----	-LARGDCCTNYQVV 137	
Db 284	KYELDGICIECTPSRKIFNHKTGRLVETNPDGRYQNGNHCYKECPPELLEENDVCVRH---	340		
Qy 138	CKGESHW- VDD--DCEEIIKAECPAGFVRPPLIIFSVGDGRASYMKGSKVMPIEKLR 193			
Db 341	CSDGHHYDATKDVRCECKRSSSCP-----	386		
Qy 194	SCGTHSPYMPRVYPTKTFPNLYTLAT-GLYPESHGIVGNSMYDPVFDATEFH-LRGREKFN 251			
Db 387	HRWGCG-----	480		
Qy 252	QPLWITATKQGVKAGTEFWSVVIPHERRLTILRWLTLPDHERPSVY 304			
Db 443	VRWALAIYQCDDEELSLNSLKL-IKIG-----	480		
Qy 305	AFYSEQOPDFSGHKYGPFGPEESSYGSPEFTPAPRKPKRQERPVAPPKKRKKRKH 364			
Db 481	-YVSKIDWSS-----	508		
Qy 365	MDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKRLRRCVNVFLFVGDHGMEDVTCDRTEF 424			
Db 509	-DSKLCETEQ-----	590		
Qy 425	LSNYLTNVDDITLVPGTLGRIRSKFSNNA-KYDPKALLAN-----	-LTCKKPQDHFKPY 476		
Db 543	WKSVGTCVEKC-----	542		
Qy 477	LKQHLPKRLHYAN-NRRIEDIHLVERRWHVARKPL-----	-DVYKPKSGKCFQGDHGFDNKV 533		
Db 591	-DTKGFLRNQTSMKCERCSPPECETCNGLGELDCLTCRH-----	590		
Qy 534	NSMOTVFGVG-----	542		
Db 639	-DCPVSHFPQTQKNVYCERKCHPTCYDNGCTGPDSN-----	638		
Qy 534	PTFKYKTKVPPFENIELY-----	568		
Db 689	-YENDT1FCLQSSGMNNVCVENDLPNYYISTYDTEGV 688			
Qy 569	-LGLKPAPNNGTHGSLNHLRLRTNT-FRPTMPEEVTRPNYPGIMYLQSDFD-----	616		
Db 749	VCKKCHHECDQNYHCANGQSTGCQCKKNFTVFKGDIQCVSECPKNLPPSNPANGECLDY 808			
Qy 617	-LGC-TCDD-----	651		
Db 809	-KVEPKNKLDDELNKLHTKGSTEERHLL 651			
Qy 652	GRPVLRYTRYDILYHTDFESGYSEIETMLL-----	708		
Db 866	-WTSYTVSKQAEVSSVPDHLTSCVRPD 708			
Qy 709	ASVRPNMSRICLIPSSELQTKLDRKLGAG 894			
RESULT	9			

YDT2_SCHPO	STANDARD;	PRT;	1888 AA.	QY	638 LHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFMLLW-TSYTYSKQAEVSS 696
AC 014207;				Db	798 -----RSQLEVKIAWLFFQT-FQVVVFYCEFELGNQNINVKWSLADSLISKL--LSA 845
DT 15-JUL-1998 (Rel. 36, Created)					
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
DT 15-JUL-1998 (Rel. 36, Last annotation update)					
DE HYPOTHETICAL 217.4 KDA PROTEIN C6B12.02C IN CHROMOSOME I.				QY	697 VPDHLITSCVRPDRVSPSFSONCLAYKNDKQMSYGFLFPYLSSSPEAKYDAFLVYNMVP 756
GN SPAC6B12.02C.				Db	846 GQSGGLCYR-NLRQAS-----DTTVIDTL-- 870
OS Schizosaccharomyces pombe (Fission yeast).					
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;				QY	757 MYPAFKRVNNYFQRVLV---KKYA---SERNGVNVIS---GPIF 791
OC Schizosaccharomycetales; Schizosaccharomycetaceae;				Db	871 ---FLEWSWILNHILFHVYKKYALWEQVNNSFFDLQKELSILEMEEKIWVIMTLPVF 926
OX NCBI_TAXID=4896;					
RN [1]				QY	792 DYDYDG-----LHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKC 837
RP SEQUENCE FROM N.A.				Db	927 QIGLNGTTHSPGNNSFWPLIIRVSEAFKMHKDGHNVKVVERYLRTVFLRIHFLISEWRW 986
RC STRAIN=972;				QY	838 DGPLSVSSIFI---LPHRPDNECSNSEDESKEWELMKMHATARVDIEHLSLD 889
RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;				Db	987 EDVAQILFLIOFFFSHRKENDLSEISETPTDDPFDVFK-SLDRPPNL-HVTALD 1039
RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.					
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC between the Swiss Institute of Bioinformatics and the EMBL outstation					
CC use by non-profit institutions as long as its content is in no way					
CC modified and this statement is not removed. Usage by and for commercial					
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/					
CC or send an email to license@isb-sib.ch).					
CC RESULT 10					
CC NUC1_CUNEE					
CC ID NUC1_CUNEE STANDARD; PRT; 252 AA.					
CC AC P81203; DT 15-DEC-1998 (Rel. 37, Created)					
CC CC 298531; CAB11064.1; DT 15-DEC-1998 (Rel. 37, Last sequence update)					
CC DR DR 298531; CAB11064.1; DT 15-DEC-1998 (Rel. 37, Last annotation update)					
CC KW Hypothetical protein; Transmembrane.					
CC FT TRANSMEM 697 717 POTENTIAL.					
CC FT TRANSMEM 755 775 POTENTIAL.					
CC FT TRANSMEM 866 886 POTENTIAL.					
CC FT TRANSMEM 915 935 POTENTIAL.					
CC FT TRANSMEM 977 997 POTENTIAL.					
CC FT TRANSMEM 1033 1053 POTENTIAL.					
CC FT TRANSMEM 1336 1356 POTENTIAL.					
CC FT TRANSMEM 1645 1665 POTENTIAL.					
CC FT DOMAIN 1662 1665 POLY-LEU.					
CC SQ SEQUENCE 1888 AA; 217432 MW; 8AD3BBC32397C29 CRC64;					
Query Match 2.48; Score 121; DB 1; Length 1888;					
Best Local Similarity 17.2%; Pred. No. 1.4;					
Matches 123; Conservative 101; Mismatches 223; Indels 268; Gaps 32;					
QY 327 SYGSPFTPAKPKRKVAPK----RQERPVAPPKPKRRKTHRMHDHYAAETRQDKMTNPL 381					
Db 441 SYG -----KKAKPKFLRVFARSSSHIPKMRKQMDSKKKYFSFDKESDRQV--- 486					
QY 382 REIDKIVGQLMDGLKOLKLRRCVNVTFVGDHGMEDVTCDRTEFLSNLYLTNVDDITLVPGT 441					
Db 487 --IDQVLSDWYSGKHELVQQ-----SHSYKKRPSDSKSVGNN 520					
QY 442 LGRIRSKFSENNAKYDPKAIIANLTCKKPKDQHFKPYLKQHLPKR-----LHYANNR 491					
Db 521 I-----FSVNSKKHSVNNINAKTAANNGLSHQNFSSEELLKKRKLFSLSVSYKKSK 574					
QY 492 RIEDTHLVERRWHVARKPLDVY-----KKP 517					
Db 575 KLKRTHTVHDKCQVKAV-LDHYIRDNIELNSKEREDCYEGTLAVPQVNTEIRKSSRKQ 632					
QY 518 SGKCFQGDHGFDNKVNMSOTVFVGYPKTKVPPFENIELYNVCMDDLGKPA--- 574					
Db 633 KAQRFIRDD--FD-----TVFFQSSSNPNYFTDVNPFWNIGIWSTTFRPGLSL 683					
QY 575 PNNG---THGSLNHLLR---TNTFRPTM-----PEETTRPNYP 606					
Db 684 PNNSFIKFTQG-LNSILQLDIVTHPFKSVYAFSCLFNIQDDVEKTFEKLKDFTETVLENLP 742					
QY 607 -----GIMYLQSDF-DLGCTCDDKVEPKKNKLDELNKR 637					
Db 743 YFTNSETVDLYNLLSFCSAFILHSQVSMGLVNLASSFLETYALVNDRV--SSISGLN-- 797					
Query Match 2.4%; Score 119.5; DB 1; Length 252;					
Best Local Similarity 25.0%; Pred. No. 0.13;					
Matches 65; Conservative 33; Mismatches 113; Indels 49; Gaps 15;					
QY 646 ERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFMLLWTS--YTVSKQAEVSSVP-DHILT 702					
Db 5 ESTLQFDPG---TARDFLERESVVISNRDRVASYWTGEHLTADSLLKTGDGVDRDHSK 60					

RESULT		11	
	VTNC_RABIT		
ID	VTNC_RABIT	STANDARD;	PRT;
874	MHTARVARDIEHLTLSLDFFRK	893	475 AA.
208	NEFKVKLTDVKA SGLTFFDK	227	
AC	P22458;		
DT	01-AUG-1991	(Rel. 19, Created)	
DT	01-AUG-1991	(Rel. 19, Last sequence update)	
DT	01-FEB-1996	(Rel. 33, Last annotation update)	
DE	VITRONECTIN PRECURSOR (SERUM SPREADING FACTOR) (S-PROTEIN) (GLYCOPROTEIN 66).		
DE	VTN.		
EN			

stolagus cuniculus (Rabbit).
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae;
I_TaxID=9986;

QUENCE FROM N.A., AND SEQUENCE OF 1-24.
LINE=91065939; PubMed=1701177;
B.; Komine Y.; Imanaka T.; Takano T.

monoclonal antibody EMR1a/212D recognizing site of deposition of intracellular lipid in atherosclerosis. Isolation and characterization of a cDNA clone for the antigen." ; *J Biol. Chem.* 265 : 21232-21236 (1990).

FUNCTION: VITRONECTIN IS A CELL ADHESION AND SPREADING FACTOR FOUND IN SERUM AND TISSUES. VITRONECTIN INTERACT WITH GLYCOSAMINOGLYCAN AND PROTEOGLYCANS. IS RECOGNIZED BY CERTAIN MEMBERS OF THE INTEGRIN FAMILY AND SERVES AS A CELL-TO-SUBSTRATE ADHESION MOLECULE. INHIBITOR OF THE MEMBRANE-DAMAGING EFFECT OF THE TERMINAL CYTOLYTIC COMPLEMENT PATHWAY.

DR	EMBL; M55442;	AAA31258.1;	-.
DR	PIR; A38340;	A38340.	
DR	HSSP; P45452;	1PEX.	
DR	InterPro; IPR000585;	-.	
DR	InterPro; IPR001212;	-.	
DR	Pfam; PF01033;	Somatomedin_B;	1.
DR	Pfam; PF00045;	hemopexin;	4.
DR	PRINTS; PRO0022;	SOMATOMEDINB.	
DR	PROSITE; PS00024;	HEMOPEXIN;	2.
DR	PROSITE; PS00524;	SOMATOMEDIN_B;	1.
KW	Heparin-binding; cell adhesion; Glycoprotein; Sulfatation; signal.		
ST	SIGNAL	1	19
ST	CHAIN	30	175
FT			WITTBONNECTMIN

FT DOMAIN	20	63	SOMATOMEDIN-B LIKE.
FT DOMAIN	150	287	HEMOPEXIN-LIKE 1.
FT DOMAIN	288	475	HEMOPEXIN-LIKE 2.
FT DOMAIN	366	392	GLYCOSAMINOGLYCAN BINDING REGION.
FT SITE	64	66	CELL ATTACHMENT SITE.
FT MOD_RES	75	75	SULFATATION (BY SIMILARITY).
FT MOD_RES	78	78	SULFATATION (BY SIMILARITY).
FT CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD	169	169	N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE	475 AA;	53943 MW;	D5D1F31B8C2FA12D CRC64;
Query Match	2.4%	Score 119.5; DB 1; Length 475;	
Best Local Similarity	23.1%	Pred. No. 0.29;	
Matches	118;	Conservative 50; Mismatches 195; Indels 147; Gaps 30;	
QY 46 VLSDSPWTNISSGSCKGRCFELQEAAGPPDCRCDNLCKSYTSCCHDFDELCL-KTARG --- 100			
Db 17 VLADQE----SCKDRCTEGFNAN-RKCQCDELCSYYQSCCCADYAAECKPQVTRGDVFT 69			
QY 101 -----WECTKDRCGEVRENAC----HCSEDCLARGDCCTNYQVVCKGESHW 144			
Db 70 MPEDEYGPYDYIEQTKDNASVHAQPESPTVGQEPTLSPDLQTEGGAEPTHEVPLEPEMET 129			
QY 145 VDDCEEIKAECPAGEFVRPP-----LIIFSDGFRASYMKK--GSKVM 186			
Db 130 LRPEGEDLQAGTTELGTSSASPAEEELCSGKPFDAFTDLKNGSLFAERGQYCYELDETAVR 189			
QY 187 PNIEKLRS--CGTHSP---YMRPVYPTKTF---PNLYTLATGL---YPE--SHGIVG 230			
Db 190 PGYPKLIQDWGIEGPIDAAFTTRINCQGKTYLFKGSQYWRFEDGILDPDYPRNISEGFSG 249			
QY 231 NSMYDPVFDATEFH----RGREKFNFHRWWGGQPLWITATKQ----GVKAGTFFWWS 277			
Db 250 -IPDNV-DAAFALPAHSYSGRERV-YFFKGDKYWEYQQQQPSQEECEGSSLSAVFEH 304			
QY 278 VVIPHE---RRILTIRWLTLPDHERPSVYAFYSEQPDF-SGHKYGPGPEESS---Y 328			
Db 305 FAMLHRDSWEDIKFLLFW----GRPSGGA---RQPQFISRDWHGVPGKVDAAMAGRIY 355			
QY 329 GSPFTPAKRPKRKVAPKRRQRERPVAAPPKKRQLKQLRRCCVNVIWVGDHGMEDVTCDRTEFLSNYLTVPGTLGIRSK 388			
Db 356 ISGLTPSPSAKKQ----GPYNYED----KSRRRSRKR---YRSRYGRGRSQNS-RRLSRSTI 397			
QY 389 GQLMDGLKQLKRLRCVNVIWVGDHGMEDVTCDRTEFLSNYLTVPGTLGIRSK 448			
Db 398 SRLWESSEEVSL----GPYNYED----YET-----WLKPATSEPIQSV 433			
QY 449 -FSNNAKYDPKAIIANLTCKKPDQHFKPY 476			
Db 434 YFFSGDKYYR----VNLRTQRVDTVNPPY 458			
RESULT 12			
NUC1_SCHPO			
ID NUC1_SCHPO		STANDARD;	PRT;
AC Q10480;			335 AA.
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE PROBABLE MITOCHONDRIAL NUCLEASE (EC 3.1.30.-)			
GN SPAC17C9.08.			
OS Schizosaccharomyces pombe (Fission yeast).			
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC Schizosaccharomyces.			
NCBI_TaxID=4896;			
RN SEQUENCE FROM N.A.			
RP STRAIN=972;			
RC Murphy L., McDougall R., Jones L., Simpson I., McNeil A., Harris D.,			
RA [1]			

RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY (BY
 CC SIMILARITY).
 CC -!- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM (BY SIMILARITY).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (POTENTIAL)
 CC -!- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
 CC FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC DR EMBL; X70951; CAA50290.1; -.
 CC DR EMBL; U33007; AAB64877.1; -.
 CC DR PIR; S31321; S31321.
 CC DR SGD; S0002838; YDR430C.
 CC KW Hypothetical protein.
 CC FT CONFLICT 11 18 YAAQAVR -> MPKHRPLA (IN REF. 2).
 CC SQ SEQUENCE 989 AA; 112180 MW; 6CAD2EE5A6080D9C CRC64;

Query Match 2.3%; Score 116.5; DB 1; Length 989;
 Best Local Similarity 18.5%; Pred. No. 1.3;
 Matches 159; Conservative 110; Mismatches 263; Indels 329; Gaps 46;

Qy 168 IFSVUDGRASYMKGSKVMMPNT-EKLRSCTT-HPYMPVYPTKTFPNLYTLATG- 220
 Db 67 VFSI-AFKTN-PPDSTGVPHILEHTLCGSVKYPVRSVKAFCRML-NKSLANFMNAMTGP 121

Qy 221 ---LYPES-----HGIVGNSMYDPVFDATFHLRGREKFNRWWGGQPLIMITATKQ 267
 Db 122 DYTFFPFSTTNPQDFANLRGVYLDSTLN P-----LLKQEDFDQEGRWLEHKNTDPE 174

Qy 268 GV-----KAGTFFWS-----VVIPH-----ERRILTILRWLTLPDHHERPS 302
 Db 175 NIVFGVVVNEMKQIISNANYFWSKFQQSIYPSLNNSGGDEMKTDLR----- 223

Qy 303 VYAFYSEQPDFSGHKYGPGEESYYGSPETPAKRPKRKVAPKRQERPVAPPKKRRRKI 362
 Db 224 ---YGDLJDFHHKKNYHPSNAKTFETYGN-----LPLVDTLQLQNE- 259

Qy 363 HRMDHYAAETRQDKMTNPL---REID-KIVGQ----- 390
 Db 260 -QFSGGYGKRARRDKLMLPQIDVQLKQIDTMLPPEKQTKAASMWTIGAPQDTYDT 318

Qy 391 -----LMDG-----LKQLKLRRRCVNVIYVGDHGMEDVTCDRTEFLSNYLTNVDDITL 437
 Db 319 FLLKVLGNLIMDGHSVWYQKLIESGIGLEFSVNSGVEPTTA-VNLITVGIQVSDEI 376

Qy 438 VPGTLGRI-RSKFSNNAKYDPK---AIIANLTCKKPQDQH----- 472
 Db 377 FKDTVNNNIFQNLLTEHPDRKRIDAIEQLELSKKDQKADFGQLLSSILPGWTNKIDP 436

Qy 473 FKPYLKQHLPKR---LHYANNRRIEDTHLLVERRWHVARKPLDVYKKPSGKCF---FQG 525
 DE HYPOTHETICAL 112.2 KDA PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).
 GN YDR430C OR D9461.18

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
 RN SEQUENCE FROM N.A.
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
 RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
 RA Moseley D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
 RA Winant A., Yelton M., Botstein D., Davis R.W.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 11-166 FROM N.A.; PubMed=8224861;
 RX MEDLINE=94040759;
 RA Ellis E.M., Reid G.A.;
 RT "The *Saccharomyces cerevisiae* MTS1 gene encodes a putative
 RNA-binding protein involved in mitochondrial protein targeting.";
 RL Gene 132:175-183(1993);

Qy 526 DHGFDNKVNSMQTVFGYCPTFKYKTKVPPFENIELYNM-----CD 567
 Db 482 SEEFSKSLSLDEEQT-----RLREKITALDEQDKKNIFRKGILLQEKQNEKEIDLSCLP 533

Qy 568 LLGLKPAPNGTHGSNLHLLRTNTFRPTMPEEVTRPNYPGIMYL----- 611
 Db 534 TLQIKDIPRAGDKSIEQ-KNNTM-----SRITDTN-GITYVRGKRLNDIIPPELF 584

Qy 612 -----QSDFDLGCTCDDRVEPKNKLDELNKRLHTKG-----STEERHLLYGRP 654

Db 585 YLPLFAE5LTNLGTTTESEIEDQI-----KLHTGGISTHVEVTSDPNTTEPRLLIFGFD 639

Qy 655 AVLYTRYD-----JLYHTDF-EGYSEEIFLMLLWTSYTVSKOAEVSSVPDHLTSC 704
 Db 640 GWLSLNSKTDHIFEFWSKILLEDFHKNSDKLKVIRLLASSNT-----SSVAD----- 687

Qy 705 VRPDVRVSPSPSONCLAYKNDKOMSYGLFPYPLSSSPEAKYDAFLVTNMVPMPYPAFKRV 764

Db 688 -----AGHAFAAR-----GYSAAHYRSSGAIN-----TLNGIEQLQFINRL 723

FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 870 870 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1039 1039 N-LINKED (GLCNAC. .).
 SQ SEQUENCE 1394 AA; 152791 MW; DFFCA81A40B2C7D1 CRC64;

Query Match 2.28; Score 112; DB 1; Length 1394;
 Best Local Similarity 23.8%; Pred. No. 4.1;
 Matches 49; Conservative 17; Mismatches 48; Indels 92; Gaps 15;

QY 44 PTVLSDSPWTNISGS----C-----KGRCFELQEAGPPD-CR--CDNLCKSYTS SCC 87
 Db 678 PSTCPDEQCVNSPGYSQCVPCTEGFRGWNQCLDVDECLEPNVCA NGDCSNLEG SYMCSC 737

QY 88 H-----DFDEL-----CLKTARGWCT-----KDRC----- 108
 Db 738 HKGYTRTPDHKHCRDIDECQQGNLCVNGQCKNT EGFSFRCTCGQGYQLSAAKDQ CIDE C 797

QY 109 -----GEVRNEENA----C-----HCSE--DCL----ARGDCCT---NY 134
 Db 798 QHRHLCAGHGCCRNT EGSSQCVCDQGYRASGLGD CINECLEDKSVQRGDCINTAGSY 857

QY 135 QVVCRGESHWDDD--CEEIKAAECP 158
 Db 858 DCTTCP-DGFQLDNNKTCQDINECEHP 882

NUCG_BOVIN STANDARD; PRT; 299 AA.

RESULT 15
 ID NUCG_BOVIN STANDARD; PRT; 299 AA.
 AC P38447;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).
 GN ENDOG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93342514; PubMed=7688144;
 RA Cote J., Ruiz-Carrillo A.;
 RT "Primers for mitochondrial DNA replication generated by endonuclease G.";
 RT RL Science 261:765-765(1993).
 RN [2]
 RP SEQUENCE OF 49-75.
 RC TISSUE=Liver, and Thymus;
 RX MEDLINE=88198128; PubMed=3360771;
 RA Moos M. Jr., Nguyen N.Y., Liu T.-Y.;
 RT "Reproducible high yield sequencing of proteins electrophoretically separated and transferred to an inert support.";
 RT RL J. Biol. Chem. 263:6005-6009(1988).
 RN [3]
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC TISSUE=Heart;
 RX MEDLINE=95175374; PubMed=7870594;
 RA Gerschenson M., Houniel K.L., Low R.L.;
 RT "Endonuclease G from mammalian nuclei is identical to the major endonuclease of mitochondria.";
 RT RL Nucleic Acids Res. 23:88-97(1995).
 CC -I- FUNCTION: CLEAVES DNA AT DOUBLE-STRANDED (DG) N. (DC) N AND AT SINGLE-STRANDED (DC) N TRACTS. IN ADDITION TO DEOXYRIBONUCLEASE ACTIVITIES, ALSO HAS RIBONUCLEASE (RNASE) AND RNASE H ACTIVITIES, CAPABLE OF GENERATING THE RNA PRIMERS REQUIRED BY DNA POLYMERASE GAMMA TO INITIATE REPLICATION OF MITOCHONDRIAL DNA.
 CC -I- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM.

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CC -I- SUBUNIT: HOMODIMER.
 CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -I- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES FAMILY.

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CC DR EMBL; X72802; CAA51320.1; -.
 CC DR InterPro; IPR001604; -.
 CC DR Pfam; PF01223; Endonuclease; Mitonuclease; Non_SPEC; 1.
 CC DR PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
 CC KW Hydrolase; Nuclease; Endonuclease; Mitochondrion; Transit peptide; Magnesium.
 CC FT TRANSIT 1 48 MITOCHONDRION.
 CC FT CHAIN 49 299 ENDONUCLEASE G.
 CC FT ACT_SITE 143 143 BY SIMILARITY.
 CC FT CONFLICT 172 172 H->S (IN REF. 3; PROBABLE ERROR).
 CC FT CONFLICT 264 264 H->S (IN REF. 3; PROBABLE ERROR).
 CC SQ SEQUENCE 299 AA; 32261 MW; B28FAFF56F04CFC7 CRC64;

Query Match 2.28; Score 111.5; DB 1; Length 299;
 Best Local Similarity 25.8%; Pred. No. 0.6;
 Matches 32; Conservative 24; Mismatches 41; Indels 27; Gaps 6;

Qy 741 SPEAKYDAFLVTNMPMYPAF-KRYWN---YFQRVLVKKYASERNGVNISGPPIFDYDYD 796
 Db 153 SQKAMDDTFYLNSVAPQVPHLNQNAWNNLKEVSRSLTRY---QNIVYVCTGPLP---- 203

Qy 797 GLHDTEDKIKQYVE----GSSIPVPTHYSSITSCLDFTQPADKCDGPLSVSSFEILPHR 851
 Db 204 -LPTEADGKSYVVKYQVIGKHNHVAVPTHEFKVLI-----LEAAGGQIELRSYMPNA 254

Search completed: July 19, 2001, 14:47:09
 Job time: 171 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:57 ; Search time 42.51 Seconds
(without alignments)
2847.779 Million cell updates/sec

Title: US-09-483-831-69

Perfect score: 5019
Sequence: 1 MARRSSEFOSQCIISLIFTPEAV.....RSYPEITLKLTYLHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :	SPTREMBL_16:*
1:	sp_archea;*
2:	sp_bacteria;*
3:	sp_fungi;*
4:	sp_human;*
5:	sp_invertebrate;*
6:	sp_mammal;*
7:	sp_mhc;*
8:	sp_organelle;*
9:	sp_phage;*
10:	sp_plant;*
11:	sp_rabbit;*
12:	sp_unclassified;*
13:	sp_vertetebrate;*
14:	sp_virus;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	5019	100.0	915	4	Q13827		Q13827 homo sapien
2	4681	93.3	863	4	Q13822		Q13822 homo sapien
3	4666	93.0	863	4	Q15117		Q15117 homo sapien
4	4439.5	88.5	862	11	Q9R1E6		Q9R1E6 mus musculu
5	4306	85.8	885	11	Q64610		Q64610 rattus norv
6	2084	41.5	875	11	Q63490		Q63490 rattus norv
7	2084	41.5	875	11	P97676		P97676 rattus norv
8	2081	41.5	875	11	P97675		P97675 rattus norv
9	2057.5	41.0	876	11	P70641		P70641 rattus norv
10	2040.5	40.7	875	4	O14638		O14638 homo sapien
11	1955.5	39.0	845	4	O9NPZ3		O9NPZ3 homo sapien
12	1955.5	39.0	925	4	Q9P1P6		Q9P1P6 homo sapien
13	1151	22.9	817	14	O90761		O90761 fowlpox vir
14	1151	22.9	817	14	Q9J5H1		Q9J5H1 fowlpox vir
15	646.5	12.9	457	10	Q9SU82		Q9SU82 arabidopsis
16	613	12.2	479	10	Q9FS13		Q9FS13 spinacia ol
17	612	12.2	496	10	Q9SU83		Q9SU83 arabidopsis
18	611.5	12.2	479	10	Q42974		Q42974 oryza sativ
19	610	12.2	829	5	P90754		P90754 caenorhabdi

Q9su81	arabidopsis	Q9SU81	20	609	12.1	461	10	Q9SU81
094323	schizosacch	094323	21	539.5	10.7	485	3	094323
Q9NQm9	homo sapien	Q9NQm9	22	534	10.6	251	4	Q9NQm9
088827	rattus norv	088827	23	526.5	10.5	257	11	088827
069013	zymomonas m	069013	24	522	10.4	429	2	069013
Q9y6x5	homo sapien	Q9y6x5	25	512	10.2	453	4	Q9y6x5
Q9eqg7	mus musculu	Q9eqg7	26	474.5	9.5	477	11	Q9EQG7
Q9ujag	homo sapien	Q9ujag	27	466.5	9.3	477	4	Q9UJA9
Q9pab9	xylella fas	Q9pab9	28	461	9.2	433	2	Q9PAB9
P90755	caenorhabdi	P90755	29	456.5	9.1	674	5	P90755
Q9h515	homo sapien	Q9h515	30	427	8.5	152	4	Q9H515
Q9tsb2	bos taurus	Q9tsb2	31	394.5	7.9	281	6	Q9TSB2
Q9qyy2	rattus norv	Q9qyy2	32	309.5	6.2	151	11	Q9QYY2
Q17540	caenorhabdi	Q17540	33	297.5	5.9	614	5	Q17540
Q9su80	arabidopsis	Q9su80	34	241.5	4.8	133	10	Q9su80
Q22129	caenorhabdi	Q22129	35	238	4.7	453	5	Q22129
Q14555	homo sapien	Q14555	36	234	4.7	45	4	Q14555
Q9ptu6	paralichthy	Q9ptu6	37	171	3.4	385	13	Q9PTU6
Q9rl1d5	mus musculu	Q9rl1d5	38	170.5	3.4	44	11	Q9RL1D5
Q45359	caenorhabdi	Q45359	39	163	3.2	360	5	Q45359
Q9jm99	mus musculu	Q9jm99	40	158.5	3.2	1054	11	Q9JM99
069954	streptomyce	069954	41	145.5	2.9	465	2	069954
Q55767	chilo iride	Q55767	42	142	2.8	1186	14	Q55767
Q9trd2	bos taurus	Q9trd2	43	135	2.7	32	6	Q9TRD2
Q92954	homo sapien	Q92954	44	134	2.7	1404	4	Q92954
Q9z4z4	streptomyce	Q9z4z4	45	132	2.6	462	2	Q9Z4Z4

ALIGNMENTS

RESULT 1	Q13827	PRELIMINARY;	PRT;	915 AA.
ID	Q13827			
AC	Q13827;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	AUTOTAXIN.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TUMOR;			
RX	MEDLINE=95074054; PubMed=7982964;			
RA	Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arrestad A.A.,			
RA	Sobel M.E., Liotta L.A., Stracke M.L.;			
RT	"CDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."			
RT	J. Biol. Chem. 269:30479-30484 (1994).			
RL	DR EMBL; L35594; AAA64785.1; -.			
DR	InterPro; IPR001212; -.			
DR	InterPro; IPR001604; -.			
DR	InterPro; IPR002591; -.			
PFam	PF01033; Somatomedin_B; 2.			
PFam	PF01663; Phosphodiester; 1.			
DR	PRINTS; PR00022; SOMATOMEDINB.			
DR	PROSITE; PS00524; SOMATOMEDIN_B; 2.			
DR	SMART; SMM0477; NUC; 1.			
SQ	SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;			
Query Match	100.0%	Score 5019;	DB 4;	Length 915;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Gaps 0;
Matches 915;	Conservative			

QY	1	MARRSSFQSCQIIISLFTFAVGYSICLGFATRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60
Db	1	MARRSSFQSCQIIISLFTFAVGYSICLGFATRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60
Qy	61	GRCFELQEAGPPDCRCDNLCKTARGWECTKDRCEVRNEENACHC 120

		RN [1]
		SEQUENCE FROM N.A.
		TISSUE=TESTIS;
		MEDLINE=95074054; PubMed=7982964;
	Db 61 GRCELQEAGPDCRCDDNLCKSYTSCCHDFDELCLKTARGWETKDRCGEVRNNEENACHC 120	RP
QY 121 SEDCLARGDCCNTNYQVVKGEHWDDCEEIAECPAGFVRPPLIIFSVDFRASYMK 180	RC	
Db 121 SEDCLARGDCCNTNYQVVKGEHWDDCEEIAECPAGFVRPPLIIFSVDFRASYMK 180	RX	
QY 181 KGSKVMPNIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIYGNSMYDPVFDA 240	RA	
Db 181 KGSKVMPNIEKLRSCTGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIYGNSMYDPVFDA 240	Sobel M.E., Liotta L.A., Stracke M.L.;	
	"cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."	
	J. Biol. Chem. 269:30479-30484 (1994).	
	RN [2]	
	SEQUENCE FROM N.A.	
	TISSUE=TESTIS;	
	MEDLINE=96158950; PubMed=8579579;	
	Lee H.Y., Clair T., Polymeropoulos M.H., Torres R.,	
Db . 241 TFHLRGREKFNRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTLRWLTLPDHER 300	RA	
QY 301 PSVYAFYSEQPDSFGHKYGPFGPEESSYGSPTPAKRPKRKVAPKRRQERPVAPPKKRR 360	RA	
Db 301 PSVYAFYSEQPDSFGHKYGPFGPEESSYGSPTPAKRPKRKVAPKRRQERPVAPPKKRR 360	RT	
	"Cloning, chromosomal localization, and tissue expression of autotaxin from human teratocarcinoma cells."	
	Biochem. Biophys. Res. Commun. 218:714-719(1996).	
QY 361 KIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIIFYGDHGMEDVTCD 420	RL	
Db 361 KIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIIFYGDHGMEDVTCD 420	EMBL; L46720; AAB00855.1; -.	
QY 421 RTEEFLSNYLTVNDDITLVPGLTGRIRSKFSNNAKYDPKAIIANLTCKPKDQHFKPYLKQH 480	DR	
Db 421 RTEEFLSNYLTVNDDITLVPGLTGRIRSKFSNNAKYDPKAIIANLTCKPKDQHFKPYLKQH 480	InterPro; IPR001212; -.	
QY 481 LPKRLHYANNRRIEDIHLVERRWHARKPLDVYKKPSGKCFQQGDHGFDNKVNSMOTVF 540	DR	
Db 481 LPKRLHYANNRRIEDIHLVERRWHARKPLDVYKKPSGKCFQQGDHGFDNKVNSMOTVF 540	InterPro; IPR001604; -.	
QY 541 VGYGPTFKYKTKVPPFENIELYNVMCDDLLGLKPAPEVNGTHGSLNHLLRNTFRPTMPEEV 600	DR	
Db 541 VGYGPTFKYKTKVPPFENIELYNVMCDDLLGLKPAPEVNGTHGSLNHLLRNTFRPTMPEEV 600	InterPro; IPR002591; -.	
QY 601 TRPNYPGIMYLQSDEFDLGCTCDDKVEPKPNKLDELNKRLHTKGSTEERHLLYGRPAVLRT 660	DR	
Db 601 TRPNYPGIMYLQSDEFDLGCTCDDKVEPKPNKLDELNKRLHTKGSTEERHLLYGRPAVLRT 660	Pfam; PF01033; Somatomedin_B; 2.	
QY 661 RYDILYHTDFESGYSEIIFMLLWTSYTVSKQAEVSSVPDHLTSCVRPSPFSQNCL 720	DR	
Db 661 RYDILYHTDFESGYSEIIFMLLWTSYTVSKQAEVSSVPDHLTSCVRPSPFSQNCL 720	PRINTS; PR00022; SOMATOMEDINB.	
QY 721 AYKNDQMSYGFPLPSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASER 780	DR	
Db 721 AYKNDQMSYGFPLPSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASER 780	PROSITE; PS00524; SOMATOMEDIN_B; 2.	
QY 781 NGVNVISGPIFIYDYDGHLHDTEDKIKQYVEGSSIPVPTHYSITITSCLDFTQPADKCDGP 840	DR	
Db 781 NGVNVISGPIFIYDYDGHLHDTEDKIKQYVEGSSIPVPTHYSITITSCLDFTQPADKCDGP 840	SMART; SM00477; NUC; 1.	
QY 841 LSVSSFILPHRDNEECSNSESDESKWVEELMKMHTARVDIEHLTSIDFFRKTSRYPE 900	DR	
Db 841 LSVSSFILPHRDNEECSNSESDESKWVEELMKMHTARVDIEHLTSIDFFRKTSRYPE 900	DR	
QY 901 ILTILKTYLHTYESEI 915	DR	
Db 901 ILTILKTYLHTYESEI 915	DR	
RESULT 2	DR	
ID Q13822 PRELIMINARY; FRT; 863 AA.	DR	
AC Q13822;	DR	
DT 01-NOV-1996 (TREMBLrel. 01, Created)	DR	
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DR	
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DR	
DE AUTOTAXIN-T.	DR	
GN ATX-T.	DR	
OS Homo sapiens (Human).	DR	
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.	DR	
NCBI_TaxID=9606;	DR	
OS Homo sapiens (Human).	DR	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	
NCBI_TaxID=9606;	DR	
QY 541 VGYGPTFKYKTKVPPFENIELYNVMCDDLLGLKPAPEVNGTHGSLNHLLRNTFRPTMPEEV 600	DR	
QY 489 VGYGPTFKYKTKVPPFENIELYNVMCDDLLGLKPAPEVNGTHGSLNHLLRNTFRPTMPEEV 548	DR	

QY	601	TRPNPGIMYQSDFDLGCTCDDKVEPKNNKLDLNKRLLHTKGSTEERHLLYGRPAVLYRT	660
QY	549	TRPNPGIMYQSDFDLGCTCDDKVEPKNNKLDLNKRLLHTKGSTEERHLLYGRPAVLYRT	608
QY	661	RYDILYHTDFESGYSEIFMLLWTSYTWSKQAEVSSVWPDHLTSCVRPVSPSFQNCL	720
QY	609	RYDILYHTDFESGYSEIFMLPWTWSYTWSKQAEVSSVWPDHLTSCVRPVSPSFQNCL	668
QY	721	AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMPYPAFKRWNYFORVLVKKYASER	780
QY	669	AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMPYPAFKRWNYFORVLVKKYASER	728
QY	781	NGVNISGPIFDDYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTQPADKCDGP	840
QY	729	NGVNISGPIFDDYDGLHDTEDKIKQYVEGSSIPVPTHYSIITSCLDFTQPADKCDGP	788
QY	841	LSVSSFILPHRPDNEECSNSSEDESKWEEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE	900
QY	789	LSVSSFILPHRPDNEECSNSSEDESKWEEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE	848
QY	901	ILTLKTYLHTYESEI 915	
QY	849	ILTLKTYLHTYESEI 863	
RESULT	3		
ID	Q15117	PRELIMINARY; PRT; 863 AA.	
Q15117;			
Q15117;	01-NOV-1996 (TREMBLrel. 01, Created)		
Q15117;	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
Q15117;	PHOSPHODIESTERASE I ALPHA.		
Q15117;	Homo sapiens (Human).		
Q15117;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Q15117;	NCBI_TaxID=9606;		
Q15117;	[1] SEQUENCE FROM N.A. MEDLINE=96163899; PubMed=8586446;		
Q15117;	Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J., Nakamura H., Sano K.; "Molecular cloning and chromosomal assignment of the human brain-type phosphodiesterase I/nucleotide pyrophosphatase gene (PDNP2)." Genomics 30:380-384(1995). EMBL; D45421; BAA08260.1; -.		
Q15117;	InterPro; IPR001212; -.		
Q15117;	InterPro; IPR001604; -.		
Q15117;	InterPro; IPR002591; -.		
Q15117;	Pfam; PF01033; Somatomedin_B; 2.		
Q15117;	Pfam; PF01663; Phosphodiest; 1.		
Q15117;	PRINTS; PRO0022; SOMATOMEDINB.		
Q15117;	PROSITE; PS00524; SOMATOMEDIN_B; 2.		
Q15117;	SMART; SM00477; NUC; 1.		
Q15117;	SEQUENCE 863 AA; 99040 MW; 318BA28B1CEA7A55 CRC64;		
RESULT	4		
Q9R1E6	PRELIMINARY; PRT; 862 AA.		
ID	Q9R1E6;		
Q9R1E6;	AC		
Q9R1E6;	DT 01-MAY-2000 (TREMBLrel. 13, Created)		
Q9R1E6;	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
Q9R1E6;	DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
Q9R1E6;	DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (EC 3.1.4.1).		
Q9R1E6;	NPPS2.		
Q9R1E6;	OS Mus musculus (Mouse).		
Q9R1E6;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Q9R1E6;	NCBI_TaxID=10090;		
Q9R1E6;	[1] SEQUENCE FROM N.A.		
RC	STRAIN=C57B/6;		
RA	Sano K., Piao J.-H.;		
RT	"Cloning and chromosomal assignment of mouse phosphodiesterase (PD-I alpha/autotaxin)." /nucleotide pyrophosphatase (PD-I alpha/autotaxin)."		

Db	322	-----	: : : : : : :MTNPLREIDKTVGQLMDGLKQLRHLRCVNVIVGDHG	358	Best Local Similarity 43.5%; Pred. No. 9.6e-162; Matches 386; conservative 160; Mismatches 248; Indels 94; Gaps 11;
QY	414	MEDVTCDRTEFLSNYLNVDDITLVPGTLGRRSKFSNNAKYDPKAIIANLTCKPDQHF	473	QY 57 GSCKGRCFELQEAGPPDCRCNDLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVNEEN 116	
Db	359	MEDVTCDRTEFLSNYLNVDDITLVPGTLGRRSKFSNNAKYDPKAIIANLTCKPDQHF	418	Db 53 GSCRKKCFDSSHRGLEGGCRCDSGCTDRGDCCWDFFDTCVSTQIWTCNSFRGGETLEAA 112	
QY	474	KPYLKQHLPKRLHYANNRRIEDIHLILVERRWVARKPLDVYKKPSGKCFQGDHFDNKV	533	QY 117 ACHOSEDCLARGDCCTNQVVCKGEHWVDDCCEIKAACPAGFVRPLIIFSVDFRA 176	
Db	419	KPYMKQHLPKRLHYANNRRIEDIHLILVERRWVARKPLDVYKKPSGKCFQGDHFDNKV	478	Db 113 LSCADDCLQRKDCCTDYKAVCQGEVPPWTEACASSOEQPQCPEGFDQPPVILFSMDGFRA 172	
QY	534	NSMQTVFVGYGPTFKYKTKVPPFENIELNVNCMDLLGLKAPANNGTHGSNLNHLLRTNTR	593	QY 177 SYMRKGSKVMPNIEKLRSGGTHSPYMRPVYPTKTFPNLYTTLATGLYPESHGTYGNMSMYDP 236	
Db	479	NSMQTVFVGYGPTFKYKRTKVPPFENIELNVNCMDLLGLKAPANNGTHGSNLNHLLRTNTR	538	Db 173 EYLQTWSTILLPNINKLXTCGLHSKYMRAAMYPTKTFPNHYTIVTGlyPESHGJIDNMNYDV 232	
QY	594	PTMPEEVTRPNYPGIMYLQSDFDLGLKAPANNGTHGSNLNHLLRTNTR	645	QY 237 VFDATEHLRGREKFNRHRWNGQPLWITATKOGVKAGTFEW-----SV 278	
Db	539	PTMPEEVTRPNYPGIMYLQSEFDLGCTCDDKVEPKNKLDELNKRLHTKGSTE-----	598	Db 233 YLNKNSLSSSVEKSNPawnSGQPIWLTAmyQGLKAASYYWLGSDAVNGSFPPNIYRNYSN 292	
QY	646	ERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFMLLWTSYTV	688	QY 279 VIPHERRILTLRLWLTPDHERPSVYAFYSEQPDSFGHKYQGPFGPEESSYGSPRTPAKRP 338	
Db	599	SKHENKKNLNGSVEPRKERHLLYGRPAVLYRTSYDILYHTDFESGYSEIFMLLWTSYI	658	Db 293 SVPYESRIATLQLWDLPKAERPSFYTIYVEEDSAAGHKSGPV-----SAG----- 338	
QY	689	SKQAEVSSVPDHLTSCVRPDVRSPEFSQNCLAYKNDKQMSYGFLLFPYLSSSPEAKYDA	748	QY 339 KRKVAPKRQERPVAPPKKRRRKIHRMDHYAAETRDQKMTNPLREIDKIVGQLMDGLKQL 398	
Db	659	SKQAEVSSSIEPEHLTNCVRPDVRSPEGSQNCLAYKNDKQMSYGFLLFPYLSSSPEAKYDA	718	Db 339 -----	
QY	749	FLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVISGSPIFDYDQGLHDTEDKIKQY	808	QY 399 KLRRCVNVIFVGHDHGMEDVTCDRTEFLSNLVDDITLVLPGTLGRIRSK-----FSNN 452	
Db	719	FLVTNMVPMYPAFKRVWAYFQRVLVKKYASERNGVNVISGSPIFDYDNYDGLRDTDEIEIKQY	778	Db 361 NLHNVCVNIIIVLADHGMDQTSQCDRVEYMTDYFPEI-NFMYMQGPAPRTRNIPQDFFFTFN 419	
QY	809	VEGSSIIPVPTHYSLITSCLDFTOPADKCDGPLSVSSFILPHRPDNECSNSEDSEKWK	868	QY 453 AKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLILVERRWHAULKPLD 512	
Db	779	VEGSSIIPVPTHYSLITSCLDFTOPADKCDGPLSVSSFILPHRPDNECSNSEDSEKWK	838	Db 420 S---EEIVRDLSCRKSDQHFKPYLTPDLPKRLHYAKNVRIDKVKHLMVDROLAYR---- 471	
QY	869	EELMKMHTARVRDIEHLTLSLDFFRKTSRSYPEILTLKTYLHTYESEI	915	QY 513 VYKPSGKCFQGDHGFDNKVSMSOTVFVGYGPTFKYKTPVPPFENIELNVNCMDLLGLK 572	
Db	839	EELMKMHTARVRDIEHLTLSLDFFRKTSRSYPEILTLKTYLHTYESEI	885	Db 472 -NKGSNC-EGGTHGYNNEFKSMEAIFLAHGPSFKEKTVIEPFENIEVNLCDLLHQ 528	
RESULT	6	SEQUENCE FROM N.A.		QY 573 PAPNGTHGSLNHLRLNTFRPTMPEVTRPNEYPGIMYLOQSDFDLGCTCDDKVEPKNKL 632	
Q63490	ID	PRELIMINARY;	PRT;	Db 529 PAPNGSHGSLNHLKAPPYOPSHAELSKSAGCGFTTPLPKDSLNCSC-LALOTSGQEE 587	
Q63490	AC	PRELIMINARY;	PRT;	QY 633 ELNKLHHTKG----STEERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFMLLWTSYT 687	
DT	01-NOV-1996	(TREMBLrel. 01, Created)		Db 588 QVNQRLNLGGEVSAEKTNLPGFGRPVIQKNKDHCLLYHREYVSGFGKAMKMPMWSYT 647	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		Db 688 VSKQAEVSSVPDHLTSCVRPDVRSPEFSQNCLAYKNDKQMSYGFLLFPYLSSSPEAKYD 747	
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		QY 748 AFLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVISGSPIFDYDGLHDTEDKIKQ 807	
DE	RBL3-6 ANTIGEN.			Db 648 VPKGDTSSLPTVPCDLCRADVRDPESEOKCSFYLADQNIDHGFLYPPAIAKGNNNEQYD 707	
OS	Rattus norvegicus (Rat).			QY 708 ALITSNLVPMYKEFKMMWDYFHKVLLIKYATERNGNVVSGSPIFDYNYDGHFADPEITN 767	
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;			QY 808 YVEGSSIPVPTHYSLITSCLDFTQPADKCDGPLSVSSFILPHRPDNECSNSSEDESKW 867	
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.			Db 768 YVAGTDDVVPVPTHYFVVLTSCKNKTHTPDSCPGWLDVLPFVYHRPTNESC PENKAEDLW 827	
OX	NCBI_TAXID=10116;			QY 868 VEELMRMHTARVRDIEHLTLSLDFFRKTSRSYPEILTLKTYLHTYESEI 915	
RN	[1]	SEQUENCE FROM N.A.		Db 828 VEERFKAHIAHRDVRDVELTIGLDFYQETKTOPVSEILQLKTYLPTFETII 875	
RP	STRAIN=SPRAQUE-DAWLEY; TISSUE=BRAIN;			RESULT 7	
RC	MEDLINE=9524775; PubMed=7730366;			ID P97676 PRELIMINARY; PRT; 875 AA.	
RX	Deissler H., Lottspeich F., Rajewsky M.F.;			AC P97676; PRELIMINARY; PRT; 875 AA.	
RA	"Affinity purification and cDNA cloning of rat neural differentiation			DT 01-MAY-1997 (TREMBLrel. 03, Created)	
RT	RT and tumor cell surface antigen gp130RB13-6 reveals relationship to			DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)	
RT	RT human and murine PC-1."			DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
RL	J. Biol. Chem. 270:9849-9855 (1995).			DE ALKALINE PHOSPHODIESTERASE.	
DR	DR InterPro; IPR001212; -.			OS Rattus norvegicus (Rat).	
DR	DR InterPro; IPR002591; -.				
DR	PFam; PF01033; Somatomedin_B; 2.				
DR	DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.				
DR	DR SMART; SM00477; NUC; 1.				
SQ	SEQUENCE 875 AA; 99087 MW; 9BA9FBFEF82DFBA6 CRC64;				
Query Match	41.5%	Score 2084; DB 11; Length 875;			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. [1] SEQUENCE FROM N.A. MEDLINE=97250927; PubMed=9096610;	Qy 748 AFLVTNMVPMYPAFKRVWNYFORVVLVKKAYASERNGVNVISGPIFYDGLHDTEDIKQ 807 Db 708 ALITSNLVPMPYKEFKKKMWDXFHKVLLIKYAIERNGVNVVSGPIFYDNYDGHFDAPDEITN 767
Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W., Maurice M.; "Biochemical and molecular identification of distinct forms of alkaline phosphodiesterase I expressed on the apical and basolateral plasma membrane surfaces of rat hepatocytes.", Hepatology 25:995-1002(1997). EMBL; U78788; AAB61536.1;_.	Qy 808 YVEGSSIPVPTHYSIITSCLDFTPADKCDGPLSVSSFILPHRPNESCNSSDESKW 867 Db 768 YVAGTDVPPVPTHYFVVTSCKKNKTHPDSCPGLWLDLPLFVVPHRPTNVESCPENKAEDIW 827
InterPro; IPR001212; _. InterPro; IPR002591; _. Pfam; PF01033; Somatomedin_B; 2. Pfam; PF01663; Phosphodiest; 1. PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2. SMART; SM00201; SO; 1. SEQUENCE 875 AA; 99071 MW; 4205F263E8A933EA CRC64;	Qy 868 VEELMKMHTARVRDIEHLTSLDFFRKTTSRYPEILTLKTYLHTYESEI 915 Db 828 VEERFAHIARVRDVELLTGDLFYQEKTOVSEILQLKTYLPTFETII 875
RESULT 8 P97675 PRELIMINARY; PRT; 875 AA. ID P97675 AC P97675; DT 01-MAY-1997 (TREMBLrel. 03, Created) AC P97675; DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update) AC P97675; DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	Qy 868 VEELMKMHTARVRDIEHLTSLDFFRKTTSRYPEILTLKTYLHTYESEI 915 Db 828 VEERFAHIARVRDVELLTGDLFYQEKTOVSEILQLKTYLPTFETII 875
"Biochemical and molecular identification of distinct forms of alkaline phosphodiesterase I expressed on the apical and basolateral plasma membrane surfaces of rat hepatocytes.", Hepatology 25:995-1002(1997). EMBL; U78788; AAB61536.1;_.	Qy 868 VEELMKMHTARVRDIEHLTSLDFFRKTTSRYPEILTLKTYLHTYESEI 915 Db 828 VEERFAHIARVRDVELLTGDLFYQEKTOVSEILQLKTYLPTFETII 875
InterPro; IPR001212; _. InterPro; IPR002591; _. Pfam; PF01033; Somatomedin_B; 2. Pfam; PF01663; Phosphodiest; 1. PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2. SMART; SM00201; SO; 1. SEQUENCE 875 AA; 99071 MW; 4205F263E8A933EA CRC64;	Qy 868 VEELMKMHTARVRDIEHLTSLDFFRKTTSRYPEILTLKTYLHTYESEI 915 Db 828 VEERFAHIARVRDVELLTGDLFYQEKTOVSEILQLKTYLPTFETII 875
Query Match 41.5%; Score 2084; DB 11; Length 875; Best Local Similarity 43.5%; Pred. No. 9.6e-162; Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;	Qy 868 VEELMKMHTARVRDIEHLTSLDFFRKTTSRYPEILTLKTYLHTYESEI 915 Db 828 VEERFAHIARVRDVELLTGDLFYQEKTOVSEILQLKTYLPTFETII 875
Qy 57 GSCKGRGCFFEAGPPDCRCDNLCKSYTSCTCCCHDFDELCLKTAGWECTKDRGEVRNEEN 116 Db 53 GSCRKKCFDSSHRLGCRDSCGCTDRCWDFFEDTCVKSTQIWTCSNSFRGGETRLEAA 112	Qy 57 GSCKGRGCFFEAGPPDCRCDNLCKSYTSCTCCCHDFDELCLKTAGWECTKDRGEVRNEEN 116 Db 53 GSCRKKCFDSSHRLGCRDSCGCTDRCWDFFEDTCVKSTQIWTCSNSFRGGETRLEAA 112
Qy 117 ACHCSEDCLARGDCTTNQWVCKGESHWDDCEEIKAAECPAGEVVRPLLIIFSVDGFRA 176 Db 113 LCSCADDCLQRKDCCCTDYKAVCQGEVPWVTEACASSQEPCQPEGFDQPPVILFSMDGFRA 172	Qy 117 ACHCSEDCLARGDCTTNQWVCKGESHWDDCEEIKAAECPAGEVVRPLLIIFSVDGFRA 176 Db 113 LCSCADDCLQRKDCCCTDYKAVCQGEVPWVTEACASSQEPCQPEGFDQPPVILFSMDGFRA 172
Qy 177 SYMKKGSKVMPNIEKLRSRGTHSPYMRPVYPTKTFPMLYTLATGLYPESHGIVGNMSYDP 236 Db 173 EYLQTWSTILLPNINKLKTGGLHSKYRAMAMYPTKTFPMLYTATGLYPESHGIVDIDNNMYDV 232	Qy 177 SYMKKGSKVMPNIEKLRSRGTHSPYMRPVYPTKTFPMLYTLATGLYPESHGIVGNMSYDP 236 Db 173 EYLQTWSTILLPNINKLKTGGLHSKYRAMAMYPTKTFPMLYTATGLYPESHGIVDIDNNMYDV 232
Qy 237 VFDATEFHLLGREKFNFNRWWGGQPLWITATKQGVKAGTFFW-----SV 278 Db 233 YLNKNFSSLSSVEKSNPAAWWSGQPIWLTAAMYQGILKAASYYYWPGSDDVAVNGSFNPNIYRNYSN 292	Qy 237 VFDATEFHLLGREKFNFNRWWGGQPLWITATKQGVKAGTFFW-----SV 278 Db 233 YLNKNFSSLSSVEKSNPAAWWSGQPIWLTAAMYQGILKAASYYYWPGSDDVAVNGSFNPNIYRNYSN 292
Qy 279 VIPHERRILTILRWLTLPDHHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGPFPFTPAKRP 338 Db 293 SVPYESRIATLLQWLQWLDLPKAERPSFYTIYVEEPDSAGHKSGPV----SAG---- 338	Qy 279 VIPHERRILTILRWLTLPDHHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGPFPFTPAKRP 338 Db 293 SVPYESRIATLLQWLQWLDLPKAERPSFYTIYVEEPDSAGHKSGPV----SAG---- 338
Qy 339 KRKVAPKRRQERPVAPPKKRRRKIHMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQL 398 Db 339 -----VIKALQLVDDAEGMILMEGLKQR 360	Qy 339 -----VIKALQLVDDAEGMILMEGLKQR 360
Qy 399 KLRCVCNVVIFVGDHGMEDVTCDRTEFLISNYLTINWDDITLVPGTLGRIRSK-----FSNN 452 Db 361 NLHNCVNIVLADHGMDQTSCDRVEYMTDYFPEI-NFMYQGPAPRIRTRNIPQDFFTFN 419	Qy 399 KLRCVCNVVIFVGDHGMEDVTCDRTEFLISNYLTINWDDITLVPGTLGRIRSK-----FSNN 452 Db 361 NLHNCVNIVLADHGMDQTSCDRVEYMTDYFPEI-NFMYQGPAPRIRTRNIPQDFFTFN 419
Qy 453 AKYDPKALLIANLTCKKPKDQHFKPQYLKQHLPKRHLHYANRRIEDIHLIWERRWHVARKPLD 512 Db 420 S----EEIVRDLSCRKSDQHFKPQYLTPDLPKRHLHYAKNRIDKVLMDQWMLAYR---- 471	Qy 453 AKYDPKALLIANLTCKKPKDQHFKPQYLKQHLPKRHLHYANRRIEDIHLIWERRWHVARKPLD 512 Db 420 S----EEIVRDLSCRKSDQHFKPQYLTPDLPKRHLHYAKNRIDKVLMDQWMLAYR---- 471
Qy 513 VYKKPSGKCFQGDNKVNNSMQTVFVGYGPFTFKYTKVPPFENIENLYVMCDLLGLK 572 Db 472 - -NKGSSNC-EGGTGHYNNEFKSMEAIFLAHGPSFKEKTVIEPFENIEVYNNLICDLLHQ 528	Qy 513 VYKKPSGKCFQGDNKVNNSMQTVFVGYGPFTFKYTKVPPFENIENLYVMCDLLGLK 572 Db 472 - -NKGSSNC-EGGTGHYNNEFKSMEAIFLAHGPSFKEKTVIEPFENIEVYNNLICDLLHQ 528
Qy 573 PAPNNGTHGSLNHLRTNTERTPTMPEEVTRPNEYPGIMYLYQSDFDLCGTCDDRKVEPKNKL 632 Db 529 PAPNNGSHGSLNHLKAPFYQPSHAELSXSAGCGFTTPLPKDSDLNCSC-LALQTSQQEE 587	Qy 573 PAPNNGTHGSLNHLRTNTERTPTMPEEVTRPNEYPGIMYLYQSDFDLCGTCDDRKVEPKNKL 632 Db 529 PAPNNGSHGSLNHLKAPFYQPSHAELSXSAGCGFTTPLPKDSDLNCSC-LALQTSQQEE 587
Qy 633 ELNKRLLHTKG---STEERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFLMLLWTSYT 687 Db 588 QVNQRLNLNSGGEVSATEKTNLPFGRPRVIOQKNDHCLLYHREYVSGFGKAMKMPMWSSYT 647	Qy 633 ELNKRLLHTKG---STEERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFLMLLWTSYT 687 Db 588 QVNQRLNLNSGGEVSATEKTNLPFGRPRVIOQKNDHCLLYHREYVSGFGKAMKMPMWSSYT 647
Qy 688 VSKQAEVSSVPDHLLTSCVRDVRVSPPFSQNCLAYKNDKQMSYGFPLPPYLSPEAKYD 747 Db 648 VPKGDTSSLPLPTVPCDLRADVRVPDSEOKCSFYLADQNIHDGFPLYPPAIKGNNESQYD 707	Qy 688 VSKQAEVSSVPDHLLTSCVRDVRVSPPFSQNCLAYKNDKQMSYGFPLPPYLSPEAKYD 747 Db 648 VPKGDTSSLPLPTVPCDLRADVRVPDSEOKCSFYLADQNIHDGFPLYPPAIKGNNESQYD 707

Db	339	- - - - - VIKALQLVDDDAFGMLMEGLKQR	360	QY	57	GSCKGRGCFELEQAGPPDCRCDNLCKSYTSCTCCCHDFDELCLKTARGWECKDRCGEVERNEEN	116
QY	399	KLRCVCNVIFVGMDVTCDRTEFLSNLYLTNVDDITLVPGTLGRIRSK-----FSNN	452	Db	53	GSCRKKCFDSSHRLGEGCRCDSGCTDRGDCCWDFEDTCVRSTQIWTCSFRCGETRLETA	112
Db	361	NLHNCVNIIIVLADHGMDQTSCDRVEYMTDYFPEI-NFYMYQGPAPRTRNIPQDFFEN	419	QY	117	ACHCSEDCLARGDCCNTNYQVVKGESHWYDDCEEEKAECPAGEFVRPLLIIFSVDGFRA	176
QY	453	AKYDPKAIIIANLTCKPDQHFCKPYLKQHLPKRHYANNRRIEDIHLLVERRWHAARKPLD	512	Db	113	LCSCADDCLQRDCTTDYKAVCQGEVPWYTEACASSQEPQCPEGFDQPVILFSMDGFRA	172
Db	420	S---EEIVRDLSCRKSDQHFKPYLTPDLPKRHYAKNVRIDKVHLMVDRQWLAIR----	471	QY	177	SYMKGSKVMPNIEKLRSCTGHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNNSMYDP	236
QY	513	VYKPSGKCFQGDFGDNKVNSMQTVFYGKPTFKYKTKVPPFENIELYVMCDLLGLK	572	Db	173	EYLQTWSTLNPINKLKTGHLSKYMRAYVPTKTFPNHYTIVTGYPESHGIIDNNMYDV	232
Db	472	- - NKGSSNC-EGGTHGYNNEFKSMEAIFLAHGPSFKEKTVIEPFENIEVYNLLCDLLHIQ	528	QY	237	VFDATFHLRGREKFNHRWNGQPLWITATKQGVKAGTFFW-----SV	278
QY	573	PAPPNGTHGSLNHNLLRTNTFRPTMPEEVTRPNEYPGIMYQLQSDFDLGCTDDKVEPKNKLD	632	Db	233	YLNKNFSSLSSVEKSNSPAWNSQPIWLTAAMYQGLKAASYYWPGSDAVNGSFNPNIYRNYSN	292
Db	529	PAPPNGSHGSLNHNLLKAPFYQPSHAEEELSKSAGCGFTTPLPKDSLNCS-C-LALQTSGQEE	587	QY	279	VIPHERRILTTLRWLTLPDHERPSVAFYSEQPDFSGHKYGPFGPEESSYGSPPTPAKRP	338
QY	633	ELNKRLHTK---GSTERHLLYGRPAVLYRT-YDILYHTDFESGYSEEIFMLLWTSYT	687	Db	293	SVPYESRIATLQLWDLPKAERPSFYTIYVEEPSAGHKSCPV----SAG-----	338
Db	588	QVNQRLNLRGEVSATEKTNLPGRPRVYQKKNKDHCCLLYREYVSGFGKAMKMPMWSSYT	647	QY	339	KRKVAPKRRQERPVAPPKRRRKIHRMDHYAAETRDQKMTNPLREIDKIVGQLMDGLKQL	398
QY	688	VSKQAEVSSVPDHLTSCKVRPDVRVSPSFESQNCLAYKNDKQMSYGFLEPPYLSSEPEAKYD	747	Db	339	339 -----VIKALQLVDDAEGMLMEGLKQR	360
Db	648	VPKPGDTSSLPPTPDCILRADVRVDPSESOQKCSFYLAQNDIDHGFPLYPPAIKGNNESQYD	707	QY	399	KLRRRCVNVIFVGDFHGMEDVTCDRTEFLSNLYLTNVDDITLVPGTLGRIRSK-----FSNN	452
QY	748	AFLVTTNMVPMYPAFKRVWNQFQRVLVKKYASERERNGVNVISGPIFDYYDGLLHDTEDKIKQ	807	Db	361	NLHNCSVNITVLADHGMDOTSCDRVEYMTDYPFPEI-NFYMVKQGPAPRIRTRNIPQDFFFTEN	419
Db	708	ALITSNLVPMYKEFKKMDYFHKVULLKYAIERNGVNVSQPIFDNYDGHFDAPDEITN	767	QY	453	AKYDPKAIIANLTCKPDQHFCKPYLKQHLPKRHYANNRRIEDIHLLVERRWHAARKPLD	512
QY	808	YVEGSSIYPVPHYSIILTSLDFTQPADKCDGGLSVSSFFILPHRPDNEESCSNSEDSEKW	867	Db	420	S---EEIVRDLSCRKSDQHFKPYLTPDLPKRHYAKNVRIDKVHLMVDRQWLAYR----	471
Db	768	YVAGTDVPPVPHYFVVLTSCKNKTHTPDSCPGWLDVLPPFVVPHRPTNVESCPENKAEDLW	827	QY	513	VYKPSGKCFQGDFDNKVNNSMOTVFVGYGPTFKYKTKVPPFENIELYVMCDLLGLK	572
QY	868	VEELMKMHTARVRDIEHILTSLDFFERKTTSRYPEILTLKTYLHTYESEI	915	Db	472	--NKGPVNC-EGGTGYNNEFKSMEAIFLAHGPSFKEKTVIEPFENIEVYNNLCDDLLHIQ	528
Db	828	VEERFAKIAHARVRDVELLTGLDFYQEKQTQPVSEIQLKTYLPTFETII	875	QY	573	PAPNGTHGSLNHNLLKAPFYQPSHAEEELSKSAGCGFTTPLPKDSLNCS-C-LALQTSGQEE	587
RESULT	9	P70641	PRELIMINARY; PRT;	876	AA.	Db	529
ID	P70641	PRELIMINARY;	PRT;	876	AA.	QY	633
AC	P70641;	"	"	"	"	Db	588
DT	01-FEB-1997	(TREMBLrel.	02,	Created)	"	QY	688
DT	01-FEB-1997	(TREMBLrel.	02,	Last sequence update)	"	Db	648
DT	01-MAR-2001	(TREMBLrel.	16,	Last annotation update)	"	QY	748
DE	"	"	"	"	"	Db	708
OS	Rattus norvegicus (Rat).	"	"	"	"	QY	808
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	"	"	"	"	Db	768
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	"	"	"	"	QY	867
OX	[1]	"	"	"	"	Db	828
RN	SEQUENCE FROM N.A.	"	"	"	"	QY	867
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE, PROXIMAL;	"	"	"	"	Db	828
RA	"Molecular cloning of phosphodiesterase I cDNA from rat small	"	"	"	"	QY	867
RT	RT intestine."	"	"	"	"	Db	828
RL	Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.	"	"	"	"	QY	867
DR	SMART; S000477; NUC; 1.	"	"	"	"	Db	828
DR	SEQUENCE 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	QY	867
DR	41.08; Score 2057.5; DB 11; Length 876;	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	Db	828
Query Match Homo sapiens (Human).	"	"	"	"	"	QY	867
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	Db	828
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"	"	"	"	"	QY	867
Matches 384; Conservative 159; Sequence 876 AA; D2F772C34A0C437A CRC64;	"	"	"	"	"	QY	867
Query Match Homo sapiens (Human).	"	"	"	"	"	Db	828
Best Local Similarity 43.28; Pred. No. 1.4e-159; Mismatches 251; Indels 95; Gaps 12;	"						

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AC Q9NPZ3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DJ131F15.2 (PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE 1
DE (HOMOLOGOUS TO MOUSE LY-41 ANTIGEN) (PC1, NPPS) ) (FRAGMENT).
DE PDNP1.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peck A. ;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; ALL117378; CAB99365.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
DR NON_TER 1
FT SEQUENCE 845 AA; 96844 MW; C2DD58248BDAC52E CRC64;
SQ

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Query Match 39.0%; Score 1955.5; DB 4; Length 845;
 Best Local Similarity 42.2%; Pred. No. 3e-151;
 Matches 378; Conservative 150; Mismatches 252; Indels 115; Gaps 19
 Qy 58 SCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVVRNEENA 117

Db	27	SCKGRCFE-RTFG--	-NCRCDAAACVELGNCCCLDYQETCIEPEHITWCNKFRCGEKRLTRSL	83		RA	Bozzali M., Pizzutti A., Trischitta E.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
QY	118	CHCSEDLARGDCCTNYQVVKGESHWVDDCEEIAAECPAGFVRPLIIFSVDFRAS	177		RL		
Db	84	CACSDDKDKGDCCIINSSVQGEKSWVEEPCESENERPQCAGFETPTILLESLDGFRAE	143		DR		
QY	178	YMKGSKVMPNIEKLRCSCGTHSPMVPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV	237		DR		
Db	144	YLHTWGGLLPVISKLKKCGTYTKNMMPVYPTKTFPNHYSIVTGLYPESHGIIIDNKMYPK	203		EMBL		
Qy	238	FDATEFHLRGREKFNHRWWGGQPLWITATKOGVKAGTEFW-----SVV	279		DR		
Db	204	MNASFLSKSKEKFNPEWYKGEPIWVAKYQGLSGTFFWPGSDVEINGIPFDIYKMYNGS	263		EMBL		
QY	280	IPHERRILTIIRWLTLTPDHERSVYAFYSEQPDFSGHKYGPFGPEESSYGSPPFTPAKRPK	339		DR		
Db	264	VPEFERILAVLQLWQLPKDERPHFYTLYLEEPDSSGHSYGPVSSE-----	308		EMBL		
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Db	309	309 -----VIKALQRVDGMVGMLMDGLKELN	331		EMBL		
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Db	389	FNEYEGIARNLSCREPNOHQFKPYLKHFPLPKRLHFAKSDRIEPLTFYLDPWQQLALNPSE--	446		DR		
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Db	447	RKYCG---SGFHGSDNFTNSNMQALFVGYGPGBKHGIEADTFENIEVYNLMCDLLNLTPA	502		DR		
QY	575	PNNGTHGSLNHLRLNTFRPTMPPEEVTRPNYPGIMYLQSDF-----DLGCTCDKVEPK	628		DR		
Db	503	PNNGTHGSLNHLKKNPVTPKHPKEV----HP---LVQCFTRNPRDNLGCSCNPSTLP-	554		DR		
QY	629	NKDELNKRHLTKGSTEE--RH--LLYGRPAVLRY-TRYDILYHTDFESGYSEIFFMLLW	683		DR		
Db	555	--IEDFQTQFNLTVAEERIJKHETLPYGRPRVQLQENTICLLSQHOFGMSGYSQDILMLPW	612		DR		
QY	684	TSYTVSKQAEVSSVPDHLTSCVRPDVRSFSQNCLAYKNDKOMSYGFLFPYPLSSSPE	743		DR		
Db	613	TSYTVDRNDSFST--EDEFNCLYQDFRIPLSPVHKCSFYKNNNTKVSYGFLSPQQLKNSS	670		DR		
QY	744	AKY-DAFLVTNMVPMPYPAFKRVWNYFQRVLYKKYASERNNGVNISGP1FDYDYDGLHDTE	802		DR		
Db	671	GIYSEALLTTNIVPMYQSFQVIVRYFHDTLRLRYAAERNGVNVSGPVFDEFDYDGRDSL	730		DR		
QY	803	DKIKQ--YVEGSSIPVPHYSITSLCLDFTOPADKCDGPLSVSSFILPHRPDNEESCN	859		DR		
Db	731	ENLRQKRRVIRNQEILIPTHEFIVLTSCKDTSQTPLHCEN-LDTLAFILPHRTDNNSESCV	789		DR		
QY	860	SSEDESKWVEELMKMHTARVRDIEHLTLSDFFRKTTSRSYPEILTLKTYLHTYESE	914		DR		
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DT	01-OCT-2000	(TrEMBLrel. 15, Created)			DR		
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)			DR		
DT	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)			DR		
DE	PDNPL,				DR		
OS	Homo sapiens (Human)				DR		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				DR		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				DR		
OX	NCBI_TaxID=9606;				DR		
RN	11] SEQUENCE FROM N.A.				DR		
RP	469 FNEYEGIARNLSCREPNOHQFKPYLKHFPLKRLHFAKSDRIEPLTFYLDQWQALNPS--	526			DR		

Fri Jul 20 08:32:33 2001

us-09-483-831-69.rspt

Page 12

Db 388 GYDNMFFSMRSIFVGYGPFRRGTKVPSFENVQVYNAVAEILGLRPAPNNGS 439
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Search completed: July 19, 2001, 14:46:48
Job time: 171 sec

GenCore version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:00 ; Search time 34.65 Seconds
 (without alignments)
 22.745 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
 Perfect score: 76
 Sequence: 1 YMRRPVYPTKTFPN 13

Scoring table: BL0SUM62
 Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :	A_Geneseq_0601:*	ALIGNMENTS
1:	/SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*	RESULT 1 AAY71992
2:	/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*	ID AAY71992 standard; peptide; 13 AA.
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21:	/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*	KW Autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
22:	/SIDS8/gcgdata/geneseqp/AA2001.DAT:*	KW metabolic disease; obesity; dyslipidemia; serum glucose; KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; KW type I phosphodiesterase activity; ATP Pyrophosphatase activity; KW ATPase; adenosine-5'-triphosphatase activity; KW phosphodiesterase catalytic site.
23:		XX Unidentified.
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PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX Disclosure; Page 3; 126pp; English.
 PS The present sequence is autotaxin phosphodiesterase catalyticic
 XX site. Phosphorylation of threonine residue at position 10 of this
 CC sequence is required for autotaxin to undergo autoprophorylation
 CC and exhibit phosphodiesterase and motility-stimulating activities.
 CC Autotaxin is a glycoprotein cytokine which increases
 CC insulin signalling in adipose tissue by producing substrate for
 CC adenosine receptors, resulting in inhibition of lipolysis,
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
 CC or generally any condition associated with elevated serum levels
 CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
 CC Transgenic animals that overexpress autotaxin are models for
 CC human metabolic diseases.
 XX Sequence 13 AA;

Query Match 100.0%; Score 76; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

Db 1 ymrpvypktfpn 13

RESULT 2

AAR86579 standard; Protein; 788 AA.

XX DT 28-JUN-1996 (first entry)

XX DE Autotaxin derived from teratocarcinoma N-tera 2D1 cells.

XX KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;

XX KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.

XX OS Homo sapiens.

XX PN WO9532221-A2.

XX PF 24-MAY-1995; 95WO-US06613.

XX PR 28-NOV-1994; 94US-0346455.

XX PR 25-MAY-1994; 94US-0249182.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX PD 30-NOV-1995.

XX PF 24-MAY-1995; 95WO-US06613.

XX PR 28-NOV-1994; 94US-0346455.

XX PR 25-MAY-1994; 94US-0249182.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX DR 1996-020533/02.

XX DR N-PSDB; AAT06613.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX DR 1996-020533/02.

XX DR N-PSDB; AAT06613.

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XX PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

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XX PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX DR 1996-020533/02.

XX DR N-PSDB; AAT06613.

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XX PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX DR 1996-020533/02.

XX DR N-PSDB; AAT06613.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX DR 1996-020533/02.

XX DR N-PSDB; AAT06613.

PT Autotaxin motility stimulating protein, and DNA encoding it - used

PT in cancer diagnosis and therapy

PT XX Claim 4; Page 62-65; 112pp; English.

PT XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it.

PT XX ATX is an autocrine motility stimulating protein which is present in cancer

PT XX cells. ATX stimulates both random and directed migration of melanoma

PT XX cells. The tumorous form of ATX is a secreted protein, while the

PT XX transmembrane bound form is not present in tumour cells. The cDNA

PT XX encoding this sequence can be used in a vector, to transform cells.

PT XX recombinant cells can then be used to produce the peptide sequences.

PT XX Antibodies specific for these sequences can be produced, and can be used

PT XX in cancer diagnosis and therapy. Different sites of localisation of the

PT XX protein are utilised for diagnosis and prognosis of the stages of tumour

PT XX progression. The sequences can be used in treatment methods to

PT XX advantageously block the activity of the secreted form of ATX, while

CC an autocrine motility stimulating protein which is present in cancer
 CC cells. ATX stimulates both random and directed migration of melanoma
 CC cells. The tumorous form of ATX is a secreted protein, while the
 CC transmembrane bound form is not present in tumour cells. The cDNA
 CC encoding this sequence can be used in a vector, to transform cells. The
 CC recombinant cells can then be used to produce the peptide sequences.
 CC Antibodies specific for these sequences can be produced, and can be used
 CC in cancer diagnosis and therapy. Different sites of localisation of the
 CC protein are utilised for diagnosis and prognosis of the stages of tumour
 CC progression. The sequences can be used in treatment methods to
 CC advantageously block the activity of the secreted form of ATX, while
 CC having little effect on the membrane form of ATX.

CC having little effect on the membrane form of AXT.
 XX Sequence 829 AA;
 SQ

Query Match 100.0%; Score 76; DB 17; Length 829;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
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 Db 115 ymrpvypktkfpn 127

RESULT 4
 AAY71986
 ID AAY71986 standard; Protein; 858 AA.
 XX AC AAY71986;
 XX DT 28-MAR-2001 (first entry)
 XX DE Rat autotaxin protein.
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity.

XX OS Rattus sp.
 XX FH Key
 FT Domain
 FT Location/Qualifiers
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 FT /note= "Putative transmembrane domain"
 FT Binding-site
 FT 122..124
 FT /label= RGD_binding_domain
 FT Region
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 FT /label= Epitope
 FT /note= "This region is specifically claimed in claim 10"
 FT Region
 FT 149..158
 FT /label= Epitope
 FT /note= "This region is absent in rat brain autotaxin designated
 as PD-1alpha sequence (AAY71989)"
 FT Active-site
 FT 196..208
 FT Region
 FT 585..595
 FT /label= Epitope
 FT /note= "This region is specifically claimed in claim 10"
 XX PN WO200068386-A1.
 XX PD 16-NOV-2000.
 XX PF 05-MAY-2000; 2000WO-US12402.
 XX PR 07-MAY-1999; 99US-0306979.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Kelly JD;
 PI DR WPI; 2001-007397/01.
 XX DR New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 DR N-PSDB; AAD02131.
 XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT Obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX PS Claim 1; Page 101-104; 126pp; English.
 XX CC The present sequence is rat autotaxin protein. Autotaxin is a
 CC glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic
 CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.

Query Match 100.0%; Score 76; DB 22;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRRPVYPTKTFPN 13
 |||||||
 Db 196 ymrpvypktkfpn 208

RESULT 5
 AAY71995
 ID AAY71995 standard; Protein; 858 AA.
 XX AC AAY71995;
 XX DT 28-MAR-2001 (first entry)
 XX DE Rat autotaxin variant (A93V).
 XX Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 XX Rattus sp.
 XX OS Synthetic.
 XX FN Key
 FT Misc-difference 93
 FT /note= "Wild type Ala substituted by Val"
 XX PN WO200068386-A1.
 XX PD 16-NOV-2000.
 XX PF 05-MAY-2000; 2000WO-US12402.
 XX PR 07-MAY-1999; 99US-0306979.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Kelly JD;
 PI DR WPI; 2001-007397/01.
 XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT Obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX PS Disclosure; Page -; 126pp; English.
 XX CC The present sequence is variant (A93V) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.

CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.

Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAV71986).

XX Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 Db 196 ymrpvypktfpn 208

RESULT 6

AAV71996
ID AAV71996 standard; Protein; 858 AA.

XX AC AAV71996;

XX DT 28-MAR-2001 (first entry)

XX DE Rat autotaxin variant (A194V).

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.

XX OS Rattus sp.
 OS Synthetic.

XX FH Key Location/Qualifiers
FT Misc-difference 194
FT /note= "Wild type Ala substituted by Val"

XX PN WO2000068386-A1.

XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12402.

XX PR 07-MAY-1999; 99US-0306979.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kelly JD;

XX DR WPI; 2001-007397/01.

XX PT New autotaxin Proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX Disclosure; Page - ; 126pp; English.

XX The present sequence is variant (A194V) of rat autotaxin protein.

CC Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.

CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.

Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAV71986).

XX SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 Db 196 ymrpvypktfpn 208

RESULT 7

AAV71997
ID AAV71997 standard; Protein; 858 AA.

XX AC AAV71997;

XX DT 28-MAR-2001 (first entry)

XX DE Rat autotaxin variant (S236T).

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.

XX OS Rattus sp.
 OS Synthetic.

XX FH Key Location/Qualifiers
FT Misc-difference 236
FT /note= "Wild type Ser substituted by Thr"
XX PN WO2000068386-A1.
XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12402.

XX PR 07-MAY-1999; 99US-0306979.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kelly JD;

XX DR WPI; 2001-007397/01.

XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX Disclosure; Page - ; 126pp; English.

CC The present sequence is variant (S236T) of rat autotaxin protein.

CC Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AY71986).

gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.

Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAV71986).

```

Query Match      100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.000014;
Matches 13; Conservative 0; Mismatches 0; Indels 0
Qy   1 YMRPVYPTKTFPN 13
DDB 196 ymrpvypyptktpn 208

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Query Match      100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT	8							
AAID	AAY71998	AA71998 standard; Protein; 858 AA.						
XX								
AC	AA71998;							
XX								
DT	28-MAR-2001 (first entry)							
XX								
DE	Rat autotaxin variant (R265K).							
XX								
KKW	Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitiviti							
KKW	adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic							
KKW	therapy; metabolic disease; obesity; dyslipidemia; serum gluc							
KKW	non-insulin dependent diabetes mellitus; NIDDM; transgenic an							
KKW	type I phosphodiesterase activity; ATP pyrophosphatase activi							
KKW	ATPase; adenosine-5'-triphosphatase activity; mutant; mutein;							
XX								
OS	Rattus sp.							
OS	Synthetic							

RESULT	9
AAV71999	
ID	AAV71999 standard; Protein; 858 AA.
XX	
AC	AAV71999;
XX	
DT	28-MAR-2001 (first entry)
XX	
DE	Rat autotaxin variant (S289T).
XX	
KW	Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW	adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW	therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW	non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW	type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW	ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant
XX	
OS	Rattus sp.
OS	Synthetic

Key	Location/Qualifiers
FFH	Misc-difference 265 /note= "Wild type Arg substituted by Lys"
FFT	WO200068386-A1.
FTT	16-NOV-2000..
PN	05-MAY-2000; 2000WO-US12402.
XXX	07-MAY-1999; 99US-0306979.
PPD	(ZYMO) ZYMOGENETICS INC.
XXX	
DPF	
XXX	
PRR	
XXX	
PA	

AA	Key	Location/Qualifiers
FH	Misc-difference	289
FT		/note= "Wild type Ser substituted by Thr"
XX	PN	WO200068386-A1.
XX	PD	16 - NOV - 2000 .
XX	PF	05 - MAY - 2000 ; 2000WO-US12402.
XX	PR	07 - MAY - 1999 ; 99US-0306979.
XX	PA	(ZYMO) ZYMOGENETICS INC

PPI
XXX
DDR
XXX
PPT
XXX
PSS
XXX

Kelly JD;
WPI; 2001-007397/01.

New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
Disclosure; Page - ; 126pp; English.

The present sequence is variant (R265K) of rat autotaxin protein. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic

AA
PI Kelly JD;
XX
DR WPI; 2001-007397/01.
XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
PS Disclosure; Page - ; 126pp; English.
XX
CC The present sequence is variant (S289T) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP Pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
 Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAV71986).

SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 Db 196 ymrpvypktkfpn 208

RESULT 10

ID AAV71991 standard; Protein; 859 AA.
 XX AAV71991;

AC DT 28-MAR-2001 (first entry)

DE Human autotaxin protein.

XX Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP Pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity.

OS Homo sapiens.

FH Key Domain 8..26 Location/Qualifiers
 FT Cleavage-site /note= "Putative transmembrane domain"

FT Binding-site 44..45
 FT Binding-site 123..125
 FT /label= RGD_binding_domain

FT Active-site 197..209

/note= "Putative phosphodiesterase active site"
 XX PN WO200068386-A1.

XX PD 16-NOV-2000.
 XX PF 05-MAY-2000; 2000WO-US12402.

XX PR 07-MAY-1999; 99US-0306979.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kelly JD;

XX DR WPI; 2001-007397/01.
 DR N-PSDB; AAD02133.

XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT PS Claim 27; Page 119-121; 126pp; English.

XX The present sequence is human autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for CC adenosine receptors, resulting in inhibition of lipolysis, CC decreased hepatic gluconeogenesis and serum glucose levels, and CC increased insulin sensitivity. It also inhibits differentiation CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'- triphosphatase (ATPase) and ATP Pyrophosphatase activities. CC Autotaxin and its analogues are used to stimulate glucose uptake CC by cells, particularly to reduce serum glucose levels for CC treatment of non-insulin dependent diabetes (NIDDM) in humans, CC or generally any condition associated with elevated serum levels CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). CC Transgenic animals that overexpress autotaxin are models for CC human metabolic diseases.

XX

SQ Sequence 859 AA;

Query Match 100.0%; Score 76; DB 22; Length 859;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 Db 197 ymrpvypktkfpn 209

RESULT 11

ID AAV71988 standard; Protein; 863 AA.
 XX AAV71988;

AC AC
 XX DT 28-MAR-2001 (first entry)

XX DE Human teratocarcinoma autotaxin.

XX KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP Pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity.

XX KW Homo sapiens.
 XX OS Homo sapiens.

XX FH Key Binding-site 127..129
 FT FT /label= RGD_binding_domain
 FT Active-site 201..213
 FT /note= "Autotaxin phosphodiesterase catalytic site"

XX PN WO200068386-A1.

XX PD 16-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12402.

XX PR 07-MAY-1999; 99US-0306979.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Kelly JD;

XX DR WPI; 2001-007397/01.
 DR N-PSDB; AAD02133.

XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 PT PS Claim 27; Page 108-110; 126pp; English.

The present sequence is autotaxin isolated from human teratocarcinoma cells. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities.

Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.

Sequence 863 AA;

Query Match 100.0%; Score 76; DB 22; Length 863;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRRPVYPTKTFPN 13

Db 201 ymrpvypktfpn 213

RESULT 12
 AAR86596 Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF; ID AAR86596 standard; Protein; 915 AA.
 XX melatoma cell; tumour; antibody; cancer diagnosis; therapy.
 XX Homo sapiens.
 AC OS WO9532221-A2.
 AC PN WO200068386-A1.
 DT 01-JUL-1996 (first entry)
 DE A2058 autotaxin protein.
 XX PD 30-NOV-1995.
 XX PF 24-MAY-1995; 95WO-US066613.
 XX PR 28-NOV-1994; 94US-0346455.
 XX PR 25-MAY-1994; 94US-0249182.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
 XX DR 1996-020533/02.
 DR WPI; 112pp; English.

XX Autotaxin motility stimulating protein, and DNA encoding it - used in cancer diagnosis and therapy
 PS Claim 4; Page 91-94; 112pp; English.

XX Autotaxin motility stimulating protein, and DNA encoding it - used in cancer diagnosis and therapy
 PT Autotaxin motility stimulating protein, and DNA encoding it - used in cancer diagnosis and therapy
 XX PS Claim 4; Page 91-94; 112pp; English.

CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This sequence represents the full length protein sequence of the A2058 melanoma cell line ATX protein. ATX is an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourous form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy.

Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of ATX, while having little effect on the membrane form of ATX.

XX SQ Sequence 915 AA;

Query Match 100.0%; Score 76; DB 17; Length 915;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YMRRPVYPTKTFPN 13
 Db 201 ymrpvypktfpn 213

RESULT 13
 AAY71987 Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP Pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; melanoma.

XX DE Human melanoma autotaxin.
 XX KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; KW type I phosphodiesterase activity; ATP Pyrophosphatase activity; KW ATPase; adenosine-5'-triphosphatase activity; melanoma.
 XX OS Homo sapiens.
 XX KW Homo sapiens.
 XX FT Binding-site 127..129 /label= RGD_binding_domain
 XX DT 28-MAR-2001 (first entry)
 XX DE Human melanoma autotaxin.
 XX KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; KW type I phosphodiesterase activity; ATP Pyrophosphatase activity; KW ATPase; adenosine-5'-triphosphatase activity; melanoma.
 XX OS Homo sapiens.
 XX KW Homo sapiens.
 XX FT Active-site 201..213 /note= "Autotaxin phosphodiesterase catalytic site"
 XX PN WO200068386-A1.
 XX PD 16-NOV-2000.
 XX PF 05-MAY-2000; 2000WO-US12402.
 XX PR 07-MAY-1999; 99US-0306979.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Kelly JD;
 XX DR WPI; 2001-007397/01.
 XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX PS Claim 27; Page 105-108; 126pp; English.

CC The present sequence is autotaxin isolated from human melanoma cells. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, and decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP Pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans,

CC sequences can be produced, and can be used in cancer diagnosis and CC therapy. Different sites of localisation of the protein are utilised for CC diagnosis and prognosis of the stages of tumour progression. The CC sequences can be used in treatment methods to advantageously block the CC activity of the secreted form of AXT, while having little effect on the CC membrane form of AXT.

XX Sequence 849 AA;

Query Match 93.4%; Score 71; DB 17; Length 849;
Best Local Similarity 92.3%; Pred. No. 0.00091;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YM RPVYPTKTFPN 13
Db 201 hmrvpyptkfpn 213

Search completed: July 19, 2001, 14:45:00
Job time: 208 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:54 ; Search time 25.97 Seconds

(without alignments)
38.131 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213

Perfect score: 76

Sequence: 1 YMRPVYPTKTEFPN 13

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	76	100.0	915	1	A55144	autotaxin precursor - human
2	70	92.1	885	1	A55453	N:Contains: phosphodiesterase I (EC 3.1.4.1)
3	69	90.8	96	2	A25274	C;Species: Homo sapiens (man)
4	69	90.8	300	2	A41179	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
5	69	90.8	925	1	A39216	C;Accession: A55144; A42329
6	66	86.8	905	1	A27410	A;Title: cloning of the human tumor motility-stimulating protein, autotaxin, rev
7	65	85.5	875	1	A57080	A;Reference number: A55144; MUID:95074054
8	54	71.1	493	2	S50443	A;Molecule type: mRNA
9	50	65.8	743	2	S19437	A;Residues: 1-915 <MUR>
10	49	64.5	457	2	T09932	A;Cross-references: GB:L35594; NID:9537905; PID:AAA64785.1; PID:9537906
11	49	64.5	461	2	T09933	A;Note: parts of this sequence were confirmed by peptide sequencing
12	49	64.5	829	2	T19494	R;Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cioce, V.; Schiffmann, J. Biol. Chem. 269, 30479-30484, 1994
13	48	63.2	496	2	T09931	A;Title: Identification, purification, and partial sequence analysis of autotaxin, a
14	47	61.8	479	2	T03293	A;Reference number: A42329; MUID:92129337
15	45	59.2	674	2	T19495	A;Molecule type: protein
16	44.5	58.6	316	2	S46237	A;Experimental source: A2058 melanoma cells
17	42	55.3	429	2	T33724	A;Cross-references: GDB:378346
18	41	53.9	247	2	T32514	A;Map Position: 8q22-8qter
19	41	53.9	381	2	T32520	C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
20	41	53.9	427	2	S57776	C;Keywords: EF hand; glycoprotein; phosphoprotein; phosphodiester hydrolase
21	41	53.9	433	2	B82537	F;55-98/Domain: somatomedin B homology <SBH1>
22	41	53.9	493	2	T01206	F;99-142/Domain: somatomedin B homology <SBH2>
23	41	53.9	1829	2	T24583	F;54,463,577,859/Binding site: carbohydrate (Asn) (covalent) #status predicted
24	40	52.6	174	2	S15391	F;210/Binding site: AMP (Thr) (covalent) #status predicted
25	40	52.6	205	2	G01942	Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 5.8e-05;
26	40	52.6	247	2	T45847	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27	40	52.6	346	2	JAO159	Db 201 YMRPVYPTKTEFPN 213
28	40	52.6	466	2	T06416	RESULT 2
29	40	52.6	1547	2	JQ0096	A55453

plasma cell membrane glycoprotein PC-1, brain specific - rat
N;Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A55453; JU0187
R;Narita, M.; Goji, J.; Nakamura, H.; Sano, K.
J. Biol. Chem. 269, 28235-28242, 1994
A;Title: Molecular cloning, expression, and localization of a brain-specific phosphodiesterase
A;Reference number: A55453; MUID:95050605
A;Accession: A55453
A;Molecule type: mRNA
A;Residues: 1-885 <NAR>
A;Cross-references: GB:D28560; NID:9464196; PIDN:BAA05910.1; PID:9464197
R;Narita, M.; Goji, J.; Sano, K.; Nakamura, H.
submitted to JIPID, February 1994
A;Reference number: JU0187
A;Accession: JU0187
A;Molecule type: mRNA
A;Residues: 1-66, 'Q', 68-81, 'T', 83-94, 'C', 96, 'A', 98-195, 'A', 197-514, 'E', 516-621, 'E', 623-6
A;Experimental source: strain Sprague-Dawley
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase
F;54-97/Domain: somatomedin B homology <SBH1>
F;98-141/Domain: somatomedin B homology <SBH2>
F;53,150,396,408,522,608,829/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;207/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 92.1%; Score 70; DB 1; Length 885;
Best Local Similarity 92.3%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 1 YMRFVYPTKTFPN 13
Db 198 YTRPVYPTKTFPN 210

RESULT 3
A25274 phosphodiesterase I (EC 3.1.4.1) - bovine (fragments)
N;Alternate names: 5'-exonuclease
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1988 #sequence_revision 23-Mar-1995 #text_change 21-May-1999
C;Accession: A25274; C48395; A48395; D48395
R;Culp, J.S.; Blytt, H.J.; Hermodson, M.; Butler, L.G.
J. Biol. Chem. 260, 8320-8324, 1985
A;Title: Amino acid sequence of the active site peptide of bovine intestinal 5'-nucleotidase
A;Reference number: A25274; MUID:85234541
A;Accession: A25274
A;Molecule type: protein
A;Residues: 1-61 <CUL>
R;Maruyama, E.; Iwamatsu, A.; Takashima, S.
Biochem. Mol. Biol. Int. 29, 579-586, 1993
A;Title: Purification and amino acid microsequencing of alkaline phosphodiesterase I from
A;Reference number: A48395; MUID:93250579
A;Accession: C48395
A;Molecule type: protein
A;Residues: 22-36;62-73;74-81;82-96 <MAR>
A;Experimental source: kidney
A;Note: sequence extracted from NCBI backbone (NCBIP:132415, NCBIP:131478)
A;Note: the correct order of the fragments is unknown
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: phosphoprotein; phosphoric diester hydrolase
F;39/Binding site: AMP (Thr) (covalent) #status experimental

Query Match 90.8%; Score 69; DB 2; Length 96;
Best Local Similarity 84.6%; Pred. No. 9.1e-05;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query 1 YMRFVYPTKTFPN 13
Db 30 YLRAYPTKTFPN 42

RESULT 4
A41179 protein kinase PC-1 (EC 2.7.1.-) - bovine (fragments)
N;Alternate names: MAPP; major acidic fibroblast growth factor-stimulated phosphoprotein
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-May-1992 #sequence_revision 22-Apr-1995 #text_change 30-Apr-1999
C;Accession: A41179; A49308
R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 266, 16791-16795, 1991
A;Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein
A;Reference number: A41179; MUID:91358477
A;Accession: A41179
A;Molecule type: protein
A;Residues: 1-26;36-56;59-67;68-133;134-144;145-267;268-300 <ODA>
A;Experimental source: liver
R;Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 268, 27318-27326, 1993
A;Title: The major acidic fibroblast growth factor (aFGF)-stimulated phosphoprotein f esterase activities
A;Reference number: A49308
A;Accession: A49308
A;Molecule type: protein
A;Residues: 27-35; 'X', 37-58 <OD2>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:141583)
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: glycoprotein; phosphoprotein; phosphotransferase
F;1-25/Domain: somatomedin B homology (fragment) <SBH>
F;36/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 90.8%; Score 69; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A;Note: sequence extracted from NCBI backbone (NCBIP:141583)
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: glycoprotein; phosphoprotein; phosphotransferase
F;1-25/Domain: somatomedin B homology (fragment) <SBH>
F;36/Binding site: AMP (Thr) (covalent) #status predicted

Query 2 MRPVYPTKTFPN 13
Db 28 MRPVYPTKTFPN 39

Query Match 90.8%; Score 69; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 2 MRPVYPTKTFPN 13
Db 28 MRPVYPTKTFPN 39

RESULT 5
A39216 plasma cell membrane glycoprotein PC-1 - human
N;Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C;Accession: A39216; S21706; S23587; S51030
R;Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Garson, O.M.; Goding, J.W.
J. Biol. Chem. 265, 17506-17511, 1990
A;Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule,
A;Reference number: A39216; MUID:91009202
A;Accession: A39216
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-925 <BUCK>
A;Cross-references: GB:J05654
R;Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
Arch. Biochem. Biophys. 295, 180-187, 1992
A;Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.
A;Reference number: S21706; MUID:92246539
A;Accession: S21706
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-925 <FUN1>
A;Accession: S23587
A;Molecule type: protein
A;Residues: 116-121;247-271,'X',273-275;279-280,'X',282-283;303-316;362-364,449-465;4

A;Note: it is uncertain whether Met-1 or Met-53 is the initiator
R;Bell, S.I.; Goding, J.W.
Eur. J. Biochem. 226, 433-443, 1994
A;Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph

Query	Database	Matches	Indels	Gaps	Score	Length
A; Reference number: S51030; MUID:95094801 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-80 <BEL> C; Genetics: A; Gene: GDB:PDNP1; M6S1; NPPS A; Cross-references: GDB:132615; OMIM:173335	Db	230	0	0	0	0
RESULT 7 A57080 cell surface antigen RB13-6 - rat N; Contains: phosphodiesterase I (EC 3.1.4.1) C; Species: Rattus norvegicus (Norway rat) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C; Accession: A57080 R; Deissler, H.; Lottspeich, F.; Rajewsky, M.F. J. Biol. Chem. 270, 9849-9855, 1995 A; Title: Affinity purification and cDNA cloning of rat neural differentiation and tumour A; Reference number: A57080; MUID:95247775 A; Accession: A57080 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-875 <DEI> A; Cross-references: GB:247987; PID:9806378; NID:9806379; PID:CAA88029.1; PID:g806379 C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology C; Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane #status predicted <TMM> F; 1-22/Domain: somatomedin B homology <SBH1> F; 145-188/Domain: somatomedin B homology <SBH2> F; 179,285,341,477,570,585,643,700,731,748/Binding site: carbohydrate (Asn) (covalent) #status predicted <EXT> F; 23-45/Domain: cytosolic #status predicted <CYT> F; 46-875/Domain: extracellular #status predicted <TMM> F; 51-94/Domain: somatomedin B homology <SBH> F; 95-138/Domain: somatomedin B homology <SBH2> F; 206/Binding site: AMP (Thr) (covalent) #status predicted <EXT> F; 237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status predicted <EXT> A; Molecule type: mRNA A; Residues: 1-905 <VAN> A; Cross-references: GB:J02700; NID:g200236; PID:AAA39893.1; PID:g200237 A; Note: the authors translated the codon CAG for residue 24 as Glu R; van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W. Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985 A; Title: Murine plasma membrane antigen PC-1: Molecular cloning of cDNA and analysis A; Reference number: I59055; S38354 A; Accession: I59055 A; Status: preliminary; deduced from cDNA clone A; Molecule type: mRNA A; Residues: 203-219 <RES> A; Cross-references: GB:MI2552; NID:g200234; PID:AAA39892.1; PID:g200235 R; Belli, S.I.; van Driel, I.R.; Goding, J.W. Eur. J. Biochem. 217, 421-428, 1993 A; Title: Identification and characterization of a soluble form of the plasma cell membrane A; Reference number: S38354; MUID:94039066 A; Accession: S38354 A; Status: preliminary A; Molecule type: DNA A; Residues: 35-219 <BEL> A; Cross-references: EMBL:L04516 C; Genetics: A; Introns: 62/3; 87/1; 126/1; 168/1; 188/2 C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology C; Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane #status predicted <SBH1> F; 127-170/Domain: somatomedin B homology <SBH2> F; 161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted <EXT> F; 238/Binding site: AMP (Thr) (covalent) #status predicted <EXT>	Qy	2	2	0	MRPVYPTKTFPN 13	MRPVYPTKTFPN 13
RESULT 8 A27410 Plasma cell membrane glycoprotein PC-1 - mouse N; Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1) C; Species: Mus musculus (house mouse) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000 C; Accession: A27410; I59055; S38354 R; van Driel, I.R.; Goding, J.W. J. Biol. Chem. 262, 4882-4887, 1987 A; Title: Primary structure deduced from cDNA clone A; Reference number: A27410; MUID:87165906 A; Accession: A27410 A; Molecule type: mRNA A; Residues: 1-905 <VAN> A; Cross-references: GB:J02700; NID:g200236; PID:AAA39893.1; PID:g200237 A; Note: the authors translated the codon CAG for residue 24 as Glu R; van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W. Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985 A; Title: Murine plasma membrane antigen PC-1: Molecular cloning of cDNA and analysis A; Reference number: I59055; S38354 A; Accession: I59055 A; Status: preliminary; translated from GB/EMBL/DDJB A; Molecule type: mRNA A; Residues: 203-219 <RES> A; Cross-references: GB:MI2552; NID:g200234; PID:AAA39892.1; PID:g200235 R; Belli, S.I.; van Driel, I.R.; Goding, J.W. Eur. J. Biochem. 217, 421-428, 1993 A; Title: Identification and characterization of a soluble form of the plasma cell membrane A; Reference number: S38354; MUID:94039066 A; Accession: S38354 A; Status: preliminary A; Molecule type: DNA A; Residues: 35-219 <BEL> A; Cross-references: EMBL:L04516 C; Genetics: A; Introns: 62/3; 87/1; 126/1; 168/1; 188/2 C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology C; Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane #status predicted <SBH1> F; 86-126/Domain: somatomedin B homology <SBH2> F; 127-170/Domain: somatomedin B homology <SBH2> F; 161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted <EXT> F; 238/Binding site: AMP (Thr) (covalent) #status predicted <EXT>	Qy	2	2	MRAMYPTKTFPN 209	MRAMYPTKTFPN 209	
RESULT 8 S50443 hypothetical protein YEL016c - yeast (Saccharomyces cerevisiae) C; Species: Saccharomyces cerevisiae C; Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 29-Oct-1999 C; Accession: S50443 R; Dietrich, F.S. submitted to the EMBL Data Library, December 1994 A; Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 a A; Reference number: S50443 A; Molecule type: DNA A; Residues: 1-493 <DIE> A; Cross-references: EMBL:U18530; NID:g602367; PID:g602383; GSPDB:GN00005; MIPS:YEL016 A; Gene: YEL016c A; Map position: 5L	Qy	1	1	YMRPVYPTKTFPN 13	YMRPVYPTKTFPN 13	
RESULT 9 S19437 Query Match 71.1%; Score 54; DB 2; Length 493; Best Local Similarity 69.2%; Pred. No. 0.17; Matches 2; Mismatches 2; Indels 0; Gaps 0; Db 118 YMIPSRPTQTFPN 130	Qy	1	1	YMRPVYPTKTFPN 13	YMRPVYPTKTFPN 13	

hypothetical protein YCR026c - yeast (Saccharomyces cerevisiae)
 N; Alternate names: hypothetical protein YCR247
 C; Species: Saccharomyces cerevisiae
 C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Dec-1997
 C; Accession: S19437; S19750; S27380
 R; Pohl, F.; Richterich, P.; Wurst, H.
 submitted to the Protein Sequence Database, March 1992
 A; Reference number: S19437
 A; Accession: S19437
 A; Molecule type: DNA
 A; Residues: 1-244 <POH>
 A; Cross-references: EMBL:X59720; MIPS:YCR026C
 R; Berben, G.; Bolle, P.A.; Gilliquet, V.; Hilger, F.
 submitted to the Protein Sequence Database, March 1992
 A; Reference number: S19433
 A; Accession: S19750
 A; Molecule type: DNA
 A; Residues: 244-743 <BER>
 A; Cross-references: EMBL:X59720; MIPS:YCR026C
 R; Bolle, P.A.; Gilliquet, V.; Berben, G.; Dumont, J.; Hilger, F.
 Yeast 8, 205-213, 1992
 A; Title: The complete sequence of K3B, a 7.9 kb fragment between PGK1 and CRY1 on chromo
 A; Reference number: S22273; MUID:92245758
 A; Accession: S27380
 A; Status: not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-106, 'H', 108-119, 'F', 121-211, 'V', 213-743 <BOL>
 C; Genetics:
 A; Map position: 3R
 C; Keywords: transmembrane protein

Query Match 64.5%; Score 49; DB 2; Length 461;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 PYYPTKTFPN 13
 |||:|||
 Db 97 PVFPTMTFPN 106

RESULT 12
 T19494
 hypothetical protein C27A7.1 - Caenorhabditis elegans
 C; Species: Caenorhabditis elegans
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C; Accession: T19494
 R; Harris, B.
 submitted to the EMBL Data Library, October 1996
 A; Reference number: Z19132
 A; Accession: T19494
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-829 <WIL>
 A; Cross-references: EMBL:Z81041; PIDN:CAB02784.1; GSPDB:GN00023; CESP:C27A7.1
 A; Experimental source: clone C27A7
 C; Genetics:
 A; Gene: CESP:C27A7.1
 A; Map position: 5
 A; Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;
 T09932
 nucleotide pyrophosphatase homolog T16L4.200 - Arabidopsis thaliana
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 C; Accession: T09932
 R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, June 1999
 A; Reference number: Z16897
 A; Accession: T09932
 A; Molecule type: DNA
 A; Residues: 1-457 <BEV>
 A; Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.200
 C; Genetics:
 A; Gene: ATSP:T16L4.200
 A; Map position: 4

Query Match 64.5%; Score 49; DB 2; Length 457;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 PYYPTKTFPN 13
 |||:|||
 Db 94 PVFPTMTFPN 103

RESULT 13
 T09931
 nucleotide pyrophosphatase homolog T16L4.190 - Arabidopsis thaliana
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 C; Accession: T09931
 R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
 submitted to the Protein Sequence Database, June 1999
 A; Reference number: Z16897
 A; Accession: T09931
 A; Molecule type: DNA
 A; Residues: 1-496 <BEV>
 A; Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
 A; Experimental source: cultivar Columbia; BAC clone T16L4
 C; Genetics:
 A; Gene: ATSP:T16L4.190
 A; Map position: 4

RESULT 11
 T09933
 nucleotide pyrophosphatase homolog T16L4.210 - Arabidopsis thaliana
 C; Species: Arabidopsis thaliana (mouse-ear cress)

Query Match 63.2%; Score 48; DB 2; Length 496;
 Best Local Similarity 80.0%; Pred. No. 1.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 PVYPTKTFPN 13
 Db 146 PVFPTLTFPN 155

RESULT 14

T03293 nucleotide pyrophosphatase homolog - rice
 C; Species: *Oryza sativa* (rice)
 C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
 C; Accession: T03293
 R; Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
 submitted to the EMBL Data Library, April 1995
 A; Description: Rice early embryogenesis gene.
 A; Reference number: Z14889
 A; Accession: T03293
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-479 <HSI>
 A; Cross-references: EMBL:U25430; NID:g818848; PID:g818849
 A; Experimental source: strain Tainung 67
 C; Genetics:
 A; Note: OSE4

Query Match 61.8%; Score 47; DB 2; Length 479;
 Best Local Similarity 70.0%; Pred. No. 2.5;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 PVYPTKTFPN 13
 Db 129 PIFPTLTFPN 138

RESULT 15

T19495 hypothetical protein C27A7.3 - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
 C; Accession: T19495
 R; Harris, B.
 submitted to the EMBL Data Library, October 1996
 A; Accession: T19132
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-674 <WIL>
 A; Cross-references: EMBL:Z81041; PIDN:CAB02785.1; GSPDB:GN00023; CESP:C27A7.3
 A; Experimental source: clone C27A7
 C; Genetics:
 A; Gene: CESP:C27A7.3
 A; Map position: 5
 A; Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1

Query Match 59.2%; Score 45; DB 2; Length 674;
 Best Local Similarity 70.0%; Pred. No. 7.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 PVYPTKTFPN 13
 Db 166 PSFPSKTFPN 175

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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:47:09 ; Search time 16.91 Seconds
 (without alignments)
 26.335 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
 Perfect score: 76
 Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	69	90.8	61	1	PPD1_BOVIN	P15396 bos taurus
2	69	90.8	873	1	PC1_HUMAN	P22413 homo sapien
3	66	86.8	871	1	PC1_MOUSE	P06802 mus musculus
4	54	71.1	493	1	YEB6_YEAST	P39997 saccharomyces cerevisiae
5	50	65.8	743	1	YCR6_YEAST	P25353 saccharomyces cerevisiae
6	44.5	58.6	316	1	E13E_HORVU	Q02438 hordeum vulgare
7	42	55.3	743	1	BGAL_THEET	P77989 thermomoanaerobacter
8	40	52.6	174	1	CRA2_HOMGA	P80007 homarus gammarus
9	40	52.6	205	1	MD21_HUMAN	Q13257 homo sapien
10	40	52.6	205	1	MD21_MOUSE	Q9z1b5 mus musculus
11	40	52.6	346	1	CYSL_LYCES	P20721 lycopersicon esculentum
12	40	52.6	1547	1	RPO_PMV	P20951 papaya mosaica
13	39	51.3	595	1	HMD2_SOLTU	Q41437 solanum tuberosum
14	39	51.3	890	1	YCF2_MESVI	Q9mup8 mesostigma
15	39	51.3	1064	1	KIN1_YEAST	P13185 saccharomyces cerevisiae
16	38	50.0	172	1	CH18_DROME	P07184 drosophila melanogaster
17	38	50.0	604	1	HMDH_NICSY	Q01559 nicotiana sylvestris
18	37	48.7	177	1	CRAB_SQUAC	P02512 squalius acanthias
19	37	48.7	232	1	HB23_MOUSE	P04231 mus musculus
20	37	48.7	264	1	HB21_MOUSE	P04230 mus musculus
21	37	48.7	264	1	HB22_MOUSE	P01915 mus musculus
22	37	48.7	264	1	HB24_MOUSE	P20040 mus musculus
23	37	48.7	264	1	HB21_MOUSE	P18468 mus musculus
24	37	48.7	264	1	HB2J_MOUSE	P18469 mus musculus
25	37	48.7	328	1	GPT_SULAC	P39465 sulfolobus solfataricus
26	37	48.7	333	1	PAP2_VACCC	P21033 vaccinia virus
27	37	48.7	333	1	PAP2_VACCV	P07617 vaccinia virus
28	37	48.7	333	1	PAP2_VARV	P33052 variola virus
29	37	48.7	480	1	SYFA_METU	Q57911 methanococcus marcusii
30	37	48.7	602	1	HMD2_LYCES	P48022 lycopersicon esculentum
31	37	48.7	636	1	UBA2 YEAST	P52488 saccharomyces cerevisiae
32	37	48.7	3358	1	PGCV_MOUSE	Q62059 mus musculus
33	37	48.7	3866	1	HRX_MOUSE	P55200 mus musculus

ALIGNMENTS

RESULT 1	PPD1_BOVIN	STANDARD;	PRT;	61 AA.
ID	PPD1_BOVIN			
AC	P15396;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE)			
DE	PHOSPHODIESTERASE (FRAGMENT).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.			
NCBI_TaxID	9913;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE-Intestine;			
RE	MEDLINE-85234541; PubMed-29899287;			
RA	Culp J.S., Blytt H.J., Hermodson M., Butler L.G.;			
RT	"Amino acid sequence of the active site peptide of bovine intestinal 5'-nucleotide phosphodiesterase and identification of the active site residue as threonine."			
RT	J. Biol. Chem. 260:8320-8324 (1985).			
RL	-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED OLIGO-NUCLEOTIDES.			
FT	PIR; A25274; A25274.			
KW	Hydrolyase.			
FT	NON_TER			
FT	ACT_SITE			
FT	SEQUENCE			
SO	61 AA.; 39 MW; 580C8B4807A61C84 CRC64;			
Query Match	90.8%	Score 69; DB 1;	Length 61;	
Best Local Similarity	84.6%	Pred. No. 1.9e-05;		
Matches	11; Conservative	1; Mismatches	1; Indels	0; Gaps 0;
QY	1 YMRRPVYPTKTFPN 13.			
DB	1:1:1:1:1:1:1			
30 YLRPAPYPTKTFPN 42				
RESULT 2				
PC1_HUMAN		STANDARD;	PRT;	873 AA.
ID	PC1_HUMAN			
AC	P22413; Q9Y6K3; Q9UP61;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 (INCLUDES: ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE (EC 3.6.1.9) (NPPASE)).			
DE	PDNP1 OR PC1 OR NPPS.			
GN	Human.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Catarrhini; Primates; Catarrhini; Hominoidea; Homo.			

OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=91009202; PubMed=2211644;
 RX Buckley M.F., Loveland K.A., McKinstry W.J., Garson O.M., Goding J.W.;
 RA "Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human
 molecule, amino acid sequence, and chromosomal location.";
 RT J. Biol. Chem. 265:17506-17511(1990).
 RL [2] SEQUENCE FROM N.A. PubMed=1315502;
 RX MEDLINE=92246539; PubMed=10480624;
 RA Funakoshi T., Kato H., Horie K., Yano T., Hori Y., Kobayashi H.,
 RA Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,
 RA Yamashina I.;
 RT "Molecular cloning of cDNAs for human fibroblast nucleotide
 pyrophosphatase.";
 RL Arch. Biochem. Biophys. 295:180-187(1992).
 RN [3] SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.
 RP MEDLINE=9408501; PubMed=10480624;
 RA Pizzuti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,
 RA Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,
 RA Tassi V., Trischitta V.;
 RT "A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding
 region is strongly associated with insulin resistance.";
 RT Diabetes 48:1881-1884(1999).
 CC -!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
 CC -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 CC -!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
 CC OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
 CC OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.
 CC -!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.

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CC DR EMBL; M57736; AAA63237.1; -.
 DR EMBL; D12485; BAA02054.1; -.
 DR EMBL; D12485; BAA02053.1; ALT_INIT.
 DR EMBL; AF067177; AAD38420.1; -.
 DR EMBL; AF067178; AAD38421.1; -.
 DR PIR; A39216; A39216.
 DR MIM; 173335; -.
 DR InterPro; IPR001212; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01663; Phosphodiest; 1.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR PRINTS; PR00022; SOMATOMEDINB.
 DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
 KW Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase;
 KW Polymorphism.
 FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT TRANSMEM 25 45 EXTRACELLULAR (POTENTIAL) SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 46 873 SOMATOMEDIN-B LIKE.
 FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.
 FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 425 425 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 533 533 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 679 679 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 696 696 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 121 121 K > Q.
 /FTId=VAR_008873.

Query Match 90.8%; Score 69; DB 1; Length 873;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MRPVYPTKTFPN 13
 Db 196 MRPVYPTKTFPN 207

RESULT 3
 PC1_MOUSE STANDARD; PRT; 871 AA.
 ID PC1_MOUSE STANDARD; PRT; 871 AA.
 AC P06802;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
 DE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
 DE (EC 3.6.1.9) (NPPASE)].
 GN PDNP1 OR PC1 OR NPPS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=87165906; PubMed=3104326;
 RX van Driel I.R., Goding J.W.;
 RA "Plasma cell membrane glycoprotein PC-1. Primary structure deduced
 RT from cDNA clones.";
 RT J. Biol. Chem. 262:4882-4887(1987).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=85056299; PubMed=3917281;
 RA Stearne P.A., van Driel I.R., Grego B., Simpson R.J., Goding J.W.;
 RA "The murine plasma cell antigen PC-1: purification and partial amino
 acid sequence.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:8619-8623(1985).
 RL J. Immunol. 134:443-448(1985).
 RN [3]
 RP FUNCTION, AND SEQUENCE FROM N.A.
 RX MEDLINE=91271356; PubMed=1647027;
 RA Rebbé N.F., Tong B.D., Finley E.M., Hickman S.;
 RA "Identification of nucleotide pyrophosphatase/alkaline
 phosphodiesterase I activity associated with the mouse plasma cell
 differentiation antigen PC-1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:5192-5196(1991).
 RN [4]
 RP SEQUENCE OF 169-185 FROM N.A.
 RX MEDLINE=86094275; PubMed=3001713;
 RA van Driel I.R., Wilks A.F., Pietersz G.A., Goding J.W.;
 RA "Murine Plasma cell membrane antigen PC-1: molecular cloning of cDNA
 and analysis of expression.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:8619-8623(1985).
 CC -!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
 CC -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 CC -!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC OLIGO-NUCLEOTIDES.
 CC -!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF
 CC ANTI BODY-SECRETING CELLS.
 CC -!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.

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DR J02700; AAA39893.1; ALT_INIT.

DR M12552; AAA39892.1; -.

DR A27410; A27410.

DR MGI:97370; Pdnpl.

DR InterPro; IPR001212; -.

DR IPR002591; -.

DR PFam; PF01663; Phosphodiest; 1.

DR PFam; PF01033; Somatomedin_B; 2.

DR PRINTS; PR00022; SOMATOMEDINB.

DR PROSITE; PS00524; SOMATOMEDIN_B; 2.

DR Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase.

DR MOD_RES ?1 BLOCKED.

FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DOMAIN 46 871 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.

FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.

FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 871 AA; 99487 MW; 80848F81071F70AA CRC64;

Query Match 86.8%; Score 66; DB 1; Length 871;

Best Local Similarity 91.7%; Pred. No. 0.001; Indels 0; Gaps 0;

QY 2 MRPVVPTKTFPN 13

Db 196 MRPMYPTKTFPN 207

RESULT 4 YEB6_YEAST

ID YEB6_YEAST STANDARD;

PRT; 493 AA.

AC P39997;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE HYPOTHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION.

GN YEL016C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Carpenter J., Chen E., Cherry J.M., Guzman E., Hartzell G., Hunicke-Smith S., Komp C., Lashkari D., Lew H., Lin D., Moesel D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: TO YEAST YCR26C.

CC DR EMBL; X59720; CAA42318.1; -.

CC DR PIR; S19437; S19437.

CC DR PIR; S27380; S27380.

CC DR SGD; S0000621; YCR026C.

CC DR InterPro; IPR002591; -.

CC DR Pfam; PF01663; Phosphodiest; 1.

CC KW Hypothetical protein; Transmembrane.

CC FT TRANSMEM 114 135 POTENTIAL.

CC SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

CC CC -!- SIMILARITY: TO YEAST YCR26C.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC CC -!- SIMILARITY: TO YEAST YEL016C.

CC DR DR PIR; S19437; S19437.

CC DR DR PIR; S27380; S27380.

CC DR DR SGD; S0000621; YCR026C.

CC DR DR InterPro; IPR002591; -.

CC DR DR Pfam; PF01663; Phosphodiest; 1.

CC KW Hypothetical protein; Transmembrane.

CC FT TRANSMEM 114 135 POTENTIAL.

CC SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

CC CC -!- SIMILARITY: TO YEAST YCR26C.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC CC -!- SIMILARITY: TO YEAST YEL016C.

CC DR DR PIR; S19437; S19437.

CC DR DR PIR; S27380; S27380.

CC DR DR SGD; S0000621; YCR026C.

CC DR DR InterPro; IPR002591; -.

CC DR DR Pfam; PF01663; Phosphodiest; 1.

CC KW Hypothetical protein; Transmembrane.

CC FT TRANSMEM 114 135 POTENTIAL.

CC SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

CC CC -!- SIMILARITY: TO YEAST YCR26C.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC CC -!- SIMILARITY: TO YEAST YEL016C.

CC DR DR PIR; S19437; S19437.

CC DR DR PIR; S27380; S27380.

CC DR DR SGD; S0000621; YCR026C.

CC DR DR InterPro; IPR002591; -.

CC DR DR Pfam; PF01663; Phosphodiest; 1.

CC KW Hypothetical protein; Transmembrane.

CC FT TRANSMEM 114 135 POTENTIAL.

CC SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

CC CC -!- SIMILARITY: TO YEAST YCR26C.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC CC -!- SIMILARITY: TO YEAST YEL016C.

CC DR DR PIR; S19437; S19437.

CC DR DR PIR; S27380; S27380.

CC DR DR SGD; S0000621; YCR026C.

CC DR DR InterPro; IPR002591; -.

CC DR DR Pfam; PF01663; Phosphodiest; 1.

CC KW Hypothetical protein; Transmembrane.

CC FT TRANSMEM 114 135 POTENTIAL.

CC SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

CC CC -!- SIMILARITY: TO YEAST YCR26C.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC CC -!- SIMILARITY: TO YEAST YEL016C.

CC DR DR PIR; S19437; S19437.

CC DR DR PIR; S27380; S27380.

CC DR DR SGD; S0000621; YCR026C.

CC DR DR InterPro; IPR002591; -.

CC DR DR Pfam; PF01663; Phosphodiest; 1.

CC KW Hypothetical protein; Transmembrane.

CC FT TRANSMEM 114 135 POTENTIAL.

CC SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

CC CC -!- SIMILARITY: TO YEAST YCR26C.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC CC -!- SIMILARITY: TO YEAST YEL016C.

CC DR DR PIR; S19437; S19437.

CC DR DR PIR; S27380; S27380.

CC DR DR SGD; S0000621; YCR026C.

CC DR DR InterPro; IPR002591; -.

CC DR DR Pfam; PF01663; Phosphodiest; 1.

CC KW Hypothetical protein; Transmembrane.

CC FT TRANSMEM 114 135 POTENTIAL.

CC SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

CC CC -!- SIMILARITY: TO YEAST YCR26C.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

RESULT 6

E13E_HORVU STANDARD; PRT; 316 AA.

ID E13E_HORVU

AC Q02438;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE GV (EC 3.2.1.39) ((1->3)-BETA-GLUCAN ENDOHYDROLASE GV) ((1->3)-BETA-GLUCANASE ISOENZYME GV) (BETA-1,3-ENDOGLUCANASE GV).

DE Hordium vulgare (Barley).

OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

OC

OX NCBI_TAXID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. CLIPPER; TISSUE=Root, and Leaf;

RX MEDLINE=94307426; PubMed=8034043;

RA Xu P., Harvey A.J., Fincher G.B.;

RT "Evolution and differential expression of the (1-->3)-beta-glucan endohydrolase-encoding gene family in barley, *Hordeum vulgare*.";

RT (1-->3)-beta-glucanase isoenzyme GV. ";

RL FEBS Lett. 348:206-210(1994).

RN [2]

RP SEQUENCE OF 5-316 FROM N.A.

RC STRAIN=CV. CLIPPER; TISSUE=Root, and Leaf;

RX MEDLINE=93013030; PubMed=1398132;

RA Xu P., Wang J., Fincher G.B.;

RT "Evolution and differential expression of the (1-->3)-beta-glucan endohydrolase-encoding gene family in barley, *Hordeum vulgare*.";

RL Gene 120:157-165(1992).

CC -!- FUNCTION: MAY PROVIDE A DEGREE OF PROTECTION AGAINST MICROBIAL INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE FUNGAL CELL WALL POLYSACCHARIDES.

CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES IN 1,3-BETA-D-GLUCANS.

CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

CC -!- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.

CC

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CC EMBL; M96939; AAA21564.1; -.

DR PIR; JC1438; JC1438.

DR HSSP; P15737; 1GHS.

DR InterPro; IPR000490; -.

DR Pfam; PF00332; GLYCO_hydro_17; 1.

DR PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.

KW Hydrolase; Glycosidase; Multigene family.

FT ACT_SITE 239 239 NUCLEOPHILE (BY SIMILARITY).

FT ACT_SITE 296 296 PROTON DONOR (BY SIMILARITY).

SQ SEQUENCE 316 AA; 34413 MW; OCC0AA9D48269B4F CRC64;

CC

RP SEQUENCE.

Best Local Similarity 81.8%; Pred. No. 1.7;

Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 RPVYPTKTFPN 13

DB 307 QPVYPT-TFPN 316

RESULT 7

BGAL_THEET STANDARD; PRT; 743 AA.

ID BGAL_THEET

AC P77989;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).

GN LACZ OR LACA.

OS Thermoanaerobacter ethanolicus (*Clostridium thermohydrosulfuricum*).

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Thermoanaerobacter group; Thermoanaerobacter.

OX NCBI_TAXID=1757;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33223 / 39E;

RA Zverlov V.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.

CC

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CC EMBL; Y08557; CAA69850.1; -.

DR InterPro; IPR001649; -.

DR Pfam; PF00703; GLYCO_hydro_2; 1.

DR PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.

DR PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.

KW Hydrolase; Glycosidase.

FT ACT_SITE 388 388 PROTON DONOR (BY SIMILARITY).

FT ACT_SITE 453 453 NUCLEOPHILE (BY SIMILARITY).

SQ SEQUENCE 743 AA; 85796 MW; FE011FF517E51DFC CRC64;

RESULT 8

CRA2_HOMGA

ID CRA2_HOMGA STANDARD; PRT; 174 AA.

AC P80007;

AC

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE CRUSTACYANIN A2 SUBUNIT.

OS Homarus gammarus (European lobster) (*Homarus vulgaris*).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Nephropoidea; Nephropidae; Homarus.

OX NCBI_TAXID=6707;

RN [1]

RP SEQUENCE.

MEDLINE=91224133; PubMed=2026162;

RA Keen J.N., Caceres I., Eliopoulos E.E., Zagalsky P.F., Findlay J.B.C.;

RA "Complete sequence and model for the A2 subunit of the carotenoid pigment complex, crustacyanin.";

RL Eur. J. Biochem. 197:407-417(1991).

CC -!- FUNCTION: BINDS THE CAROTENOID ASTAXANTHIN WHICH PROVIDES THE BLUE COLORATION TO THE CARAPACE OF THE LOBSTER.

CC -!- SUBUNIT: OLIGOMER; CAN FORM DIMERS (BETA-CRUSTACYANIN); OR COMPLEXES WITH 16 SUBUNITS (ALPHA-CRUSTACYANIN). THERE ARE FIVE TYPES OF SUBUNITS: A1, A2, A3, C1 AND C2.

CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR, CARAPACE.

CC -!- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
 DR PIR; S15391; S15391.
 DR InterPro; IPR000566; -.
 DR InterPro; IPR002345; -.
 DR InterPro; IPR003057; -.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00179; LIPOCALIN.
 DR PRINTS; PR01273; INVTRTCOLOR.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 KW Pigment; Lipocalin; Transport.
 FT DISULFID 12 119 BY SIMILARITY.
 FT DISULFID 46 170 BY SIMILARITY.
 SQ SEQUENCE 174 AA; 19670 MW; AC47FAA650C5E44E CRC64;

Query Match 52.6%; Score 40; DB 1; Length 174;
 Best Local Similarity 87.5%; Pred. No. 5.2;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VYPTKTFP 12
 ||||| | |
 Db 80 VYPTKEFP 87

RESULT 9
 ID MD21_HUMAN STANDARD; PRT; 205 AA.
 AC Q13257;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1)
 DE (HSMAD2)
 GN MAD2L1 OR MAD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] RP SEQUENCE FROM N.A.
 RX MEDLINE-96421709; PubMed-8824189;
 RA Li Y.; Benezra R.;
 RT "Identification of a human mitotic checkpoint gene: hSMAD2.";
 RL Science 274:246-248(1996).
 RN [2] RP SEQUENCE FROM N.A.
 RA Jin D.-Y.; Jeang K.-T.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
 RN [3] RP SEQUENCE FROM N.A.
 RA Kleber S.; Barnikol-Watanabe S.; Kratzin H.D.; Hilschmann N.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 RN [4] RP INTERACTION WITH CDC20.
 RX MEDLINE-98301442; PubMed-9637688;
 RA Fang G.; Yu H.; Kirschner M.W.;
 RT "The checkpoint protein MAD2 and the mitotic regulator CDC20 form a ternary complex with the anaphase-promoting complex to control anaphase initiation.";
 RL Genes Dev. 12:1871-1883(1998).
 RN [5] RP INTERACTION WITH ADAM17.
 RX PubMed-10527948;
 RA Nelson K.K.; Schlondorff J.; Blobel C.P.;
 RT "Evidence for an interaction of the metalloprotease-disintegrin tumour necrosis factor alpha convertase (TACE) with mitotic arrest deficient 2 (MAD2), and of the metalloprotease-disintegrin MDC9 with a novel MAD2-related protein, MAD2-beta.";
 RL Biochem. J. 343:673-680(1999).
 RN [6] RP STRUCTURE BY NMR OF 11-195.
 RX MEDLINE-20165182; PubMed-10700282;
 RA Luo X.; Fang G.; Coldiron M.; Lin Y.; Yu H.; Kirschner M.W.,

RA Wagner G.; "Structure of the Mad2 spindle assembly checkpoint protein and its interaction with Cdc20.";
 RT Nat. Struct. Biol. 7:224-229(2000).
 CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY SEQUESTRING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPHASE PLATE.
 CC -!- SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.

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CC DR EMBL; U65410; AAC50781.1; -.
 DR EMBL; U31278; AAC52060.1; -.
 DR EMBL; AJ000186; CAA03943.1; -.
 DR MIM; 601467; -.
 DR PDB; 1DUJ; 08-MAR-00.
 DR InterPro; IPR003511; -.
 DR Pfam; PF02301; HORMA; 1.
 KW Cell cycle; Mitosis; Nuclear protein; 3D-structure.
 SQ SEQUENCE 205 AA; 23510 MW; B8DCBFF0043836764 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 205;
 Best Local Similarity 54.5%; Pred. No. 6.2;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YMRRPVYPTKTF 11
 | | :| :| :|
 Db 33 YQRGIVYPSETF 43

RESULT 10
 ID MD21_MOUSE STANDARD; PRT; 205 AA.
 AC Q9Z1B5; Q9J153;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1).
 GN MAD2L1 OR MAD2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RC STRAIN=129;
 RC PubMed=10892650;
 RA Dobles M.; Liberal V.; Scott M.L.; Benezra R.; Sorger P.K.;
 RT "Chromosome missegregation and apoptosis in mice lacking the mitotic checkpoint protein Mad2.";
 RT Cell 101:635-645(2000).
 CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT

CC INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
CC SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
CC METAPHASE PLATE (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH CDC20.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.

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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U83902; AAD09238.1; -.
DR EMBL; AF261919; AAF69525.1; -.
DR InterPro; IPR003511; -.
DR Pfam; PF02301; HORMA; 1.
KW Cell cycle; Mitosis; Nuclear protein.
FT CONFLICT 157 157 T -> A (IN REF. 1).
FT CONFLICT 178 178 C -> S (IN REF. 1).
FT CONFLICT 201 201 T -> I (IN REF. 1).
SQ SEQUENCE 205 AA; 23598 MW; A9F3F28BC4C9738E CRC64;

Query Match 52.6%; Score 40; DB 1; Length 205;
Best Local Similarity 54.5%; Pred. No. 6.2;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YMRFVYPTKTF 11
Db 33 YORGIVYPSETF 43

RESULT 11
CYSL_LYCES
ID CYSL_LYCES
STANDARD; PRT; 346 AA.

AC P20721;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE LOW-TEMPERATURE-INDUCED CYSTEINE PROTEINASE PRECURSOR (EC 3.4.22.-)
DE (FRAGMENT).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;
OC Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; solanum.
OX NCBI_TaxID=4081;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=CV. VFNT CHERRY;
RA Schaffner M.A.; Fischer R.L.;
RT "Analysis of mRNAs that accumulate in response to low temperature
RT identifies a thiolprotease in tomato.";
RL Plant Physiol. 87:431-436(1988).
CC -!- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAPAIN FAMILY OF THIOL PROTEASES.

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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M21444; AAA66308.1; -.
DR PIR; JA0159; JA0159.
DR HSSP; P00785; 2ACT.
DR MEROPS; C01_029; -.
DR InterPro; IPR000118; -.

CC DR InterPro; IPR000169; -.
CC DR InterPro; IPR000668; -.
CC DR Pfam; PF00112; Peptidase_C1; 1.
CC DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
CC DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
CC DR PROSITE; PS00640; THIOL_PROTEASE ASN; FALSE_NEG.
KW Hydrolase; Thiol protease; Zymogen; Glycoprotein.
NON_TER 1 1
FT PROPEP <1 17
FT CHAIN 18 346
ACT_SITE 42 42
FT ACT_SITE 178 178
FT ACT_SITE 198 198
FT DISULFID 39 81
FT DISULFID 73 114
FT DISULFID 172 223
FT CARBOHYD 215 215
SQ SEQUENCE 346 AA; 37429 MW; D42AC73944010928 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 346;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 12
RRPO_PMV
ID RRPO_PMV
STANDARD; PRT; 1547 AA.

AC P20951;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (176 KDa PROTEIN) (ORF 1) [CONTAINS: RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
J. Gen. Virol. 70:2325-2331(1989).
-!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.

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CC
DR EMBL; D13957; BAA03050.1; -.
DR PIR; JQ0096; JQ0096.
DR InterPro; IPR000606; -.
DR Pfam; PF01443; Viral_helicasel; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transferase.

FT NP_BIND 822 829 ATP (POTENTIAL).
SQ SEQUENCE 1547 AA; 176320 MW; 6CA4282C6A082622 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 1547;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	6 YPTKTFN 1.3	SQ	SEQUENCE	595 AA;	63841 MW;	OFA7069849D41D57 CRC64;
Db	409 YPTKTFDN 416		Query Match	51.3%;	Score 39;	DB 1; Length 595;
			Best Local Similarity	66.7%;	Pred. No. 28;	
			Matches	6;	Conservative 2;	Mismatches 1; Indels 0; Gaps 0;
RESULT 13	HMD2_SOLTU	Db	3 RPVYPTKTF 11	9 KPVYPSKVF 17		
ID	BMD2_SOLTU		STANDARD;	PRT;	595 AA.	
AC	Q41437;					
DT	01-OCT-2000 (Rel. 40, Created)					
DT	01-OCT-2000 (Rel. 40, Last sequence update)					
DT	01-OCT-2000 (Rel. 40, Last annotation update)					
DE	3-HYDROXY-3-METHYLGLUTARYL-COEZYME A REDUCTASE 2 (EC 1.1.1.34) (HMG-COA REDUCTASE 2) (HMG2).					
GN	HMG2.					
OS	Solanum tuberosum (Potato).					
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;					
OC	"HMG-COA reductase gene families that differentially accumulate transcripts in potato tubers are developmentally expressed in floral tissues.";					
RT	Korth K.L., Stermer B.A., Bhattacharyya M.K., Dixon R.A.;					
RT	"HMG-COA reductase gene families that differentially accumulate transcripts in potato tubers are developmentally expressed in floral tissues.";					
RT	Plant Mol. Biol. 33:545-551 (1997).					
RL	SEQUENCE FROM N.A.					
RC	STRAIN=CV. KENNEBEC; TISSUE=Tuber;					
RX	MEDLINE=97201488; PubMed=9049274;					
RA	Korth K.L., Stermer B.A., Bhattacharyya M.K., Dixon R.A.;					
RT	"HMG-COA reductase gene families that differentially accumulate transcripts in potato tubers are developmentally expressed in floral tissues.";					
RT	Plant Mol. Biol. 33:545-551 (1997).					
CC	-!- FUNCTION: CATALYZES THE SYNTHESIS OF MEVALONATE. THE SPECIFIC PRECURSOR OF ALL ISOPRENOID COMPOUNDS PRESENT IN PLANTS.					
CC	-!- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) = (S)-3-HYDROXY-3-METHYLGLUTARYL-COA + 2 NADPH.					
CC	-!- PATHWAY: MEVALONATE BIOSYNTHESIS, PLANT ISOPRENOID BIOSYNTHESIS.					
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM.					
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWERS AND IN MATURE SEPARALS AND OVARIES.					
CC	-!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.					
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CC	EMBL; AF166114; AAF43852.1; -.					
CC	InterPro; IPR001081; -.					
CC	InterPro; IPR001939; -.					
CC	Pfam; PF00004; APA; 1.					
CC	PROSITE; PS00674; AAA; 1.					
DR	EMBL; U51985; AAB52551.1; -.					
DR	Mendel; 10574; Soltu; 1091; 10574.					
DR	InterPro; IPR002202; -.					
DR	Pfam; PF00368; HMG-COA_red; 1.					
DR	PRINTS; PR00071; HMGCODRTASE.					
DR	PROSITE; PS00066; HMG_COA_REDUCTASE_1; 1.					
DR	PROSITE; PS00318; HMG_COA_REDUCTASE_2; 1.					
DR	PROSITE; PS01192; HMG_COA_REDUCTASE_3; 1.					
DR	PROSITE; PS50065; HMG_COA_REDUCTASE_4; 1.					
KW	Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane; Isoprene biosynthesis; NADP; Multigene family.					
FT	DOMAIN 1 112 MEMBRANE-BOUND (BY SIMILARITY).					
FT	DOMAIN 113 183 LINKER (BY SIMILARITY).					
FT	DOMAIN 184 595 CATALYTIC (BY SIMILARITY).					
FT	TRANSMEM 48 68 POTENTIAL.					
FT	TRANSMEM 92 112 BY SIMILARITY.					
FT	ACT_SITE 278 278 BY SIMILARITY.					
FT	ACT_SITE 486 486 BY SIMILARITY.					
FT	ACT_SITE 584 584 GENERAL BASE (BY SIMILARITY).					
FT	CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 342 342 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 455 455 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 588 588 N-LINKED (GLCNAC. .) (POTENTIAL).					
RESULT 14	YCF2_MESVI	Db	3 RPVYPTKTFP 12	650 RPVYPSVKLFP 659		
ID	YCF2_MESVI		STANDARD;	PRT;	1064 AA.	
AC	Q9MUP8;					
DT	01-OCT-2000 (Rel. 40, Created)					
DT	01-OCT-2000 (Rel. 40, Last sequence update)					
DT	01-OCT-2000 (Rel. 40, Last annotation update)					
DE	HYPOTHETICAL 103.9 KDA PROTEIN YCF2 (REF2).					
GN	YCF2.					
OS	Mesostigma viride.					
OG	Chloroplast.					
OC	Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;					
OC	Chlorodendrales; Mesostigmataceae; Mesostigma.					
OX	[1]					
RN	SEQUENCE FROM N.A.					
RC	STRAIN=CV. KENNEBEC; TISSUE=Tuber;					
RX	MEDLINE=97201488; PubMed=9049274;					
RA	Korth K.L., Stermer B.A., Bhattacharyya M.K., Dixon R.A.;					
RT	"HMG-COA reductase gene families that differentially accumulate transcripts in potato tubers are developmentally expressed in floral tissues.";					
RT	Plant Mol. Biol. 33:545-551 (1997).					
CC	-!- FUNCTION: CATALYZES THE SYNTHESIS OF MEVALONATE. THE SPECIFIC PRECURSOR OF ALL ISOPRENOID COMPOUNDS PRESENT IN PLANTS.					
CC	-!- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) = (S)-3-HYDROXY-3-METHYLGLUTARYL-COA + 2 NADPH.					
CC	-!- PATHWAY: MEVALONATE BIOSYNTHESIS, PLANT ISOPRENOID BIOSYNTHESIS.					
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM.					
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWERS AND IN MATURE SEPARALS AND OVARIES.					
CC	-!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.					
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CC	EMBL; AF166114; AAF43852.1; -.					
CC	InterPro; IPR001081; -.					
CC	InterPro; IPR001939; -.					
CC	Pfam; PF00004; APA; 1.					
CC	PROSITE; PS00674; AAA; 1.					
CC	KW	Chloroplast; Hypothetical protein.				
CC	SEQUENCE 890 AA; 103935 MW; 43CAEEE991AF2C4B CRC64;					
SQ	SEQUENCE	Db	51.3%;	Score 39;	DB 1;	Length 890;
	Best Local Similarity		70.0%;	Pred. No. 43;		
	Matches		7;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
QY	3 RPVYPTKTFP 12					
ID	KIN1_YEAST	Db	51.3%;	Score 39;	DB 1;	Length 890;
AC	P13185; Q04606;					
DT	01-JAN-1990 (Rel. 13, Created)					
DT	01-NOV-1997 (Rel. 35, Last sequence update)					
DT	30-MAY-2000 (Rel. 39, Last annotation update)					
DE	PROTEIN KINASE KIN1 (EC 2.7.1.-).					
GN	KIN1 OR YDR122W OR YD9727.17.					
OS	Saccharomyces cerevisiae (Baker's yeast).					
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;					

OC Saccharomyctales; Saccharomycetaceae; Saccharomyces .
 OC NCBI_TAXID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=87317589; PubMed=2957690;

RA Levin D.E., Hammond C.I., Ralston R.O., Bishop J.M.;

RT "two yeast genes that encode unusual protein kinases." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6035-6039(1987).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RA Murphy L., Shore L., Harris D., Barrell B.G., Rajandream M.A.,

RA Walsh S.V.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN

CC KINASE.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- NIMI SUBFAMILY.

CC -!- DR M69017; AAA34722.1; -.

CC -!- DR EMBL; Z48758; CAA88675.1; -.

CC -!- DR PIR; S42438; S42438.

CC -!- DR HSSP; Q63450; 1A06.

CC -!- DR SGD; S0002529; KIN1.

CC -!- DR InterPro; IPR000719; -.

CC -!- DR InterPro; IPR002290; -.

CC -!- DR Pfam; PF00069; Pkinase; 1.

CC -!- DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

CC -!- DR PROSITE; PS550011; PROTEIN_KINASE_DOM; 1.

CC -!- KW Transferase; Serine/threonine-protein kinase; ATP-binding.

CC -!- FT DOMAIN 120 398 PROTEIN KINASE.

CC -!- FT NP_BIND 126 134 ATP (BY SIMILARITY).

CC -!- FT BINDING 149 149 ATP (BY SIMILARITY).

CC -!- FT ACT_SITE 269 269 BY SIMILARITY.

CC -!- FT CONFLICT 25 25 S -> R (IN REF. 1).

CC -!- FT CONFLICT 453 453 T -> H (IN REF. 1).

CC -!- FT CONFLICT 455 455 V -> G (IN REF. 1).

CC -!- FT CONFLICT 718 718 A -> R (IN REF. 1).

CC -!- FT CONFLICT 920 921 NI -> IN (IN REF. 1).

CC -!- FT CONFLICT 976 976 T -> A (IN REF. 1).

CC -!- FT CONFLICT 979 980 SI -> T (IN REF. 1).

CC -!- FT CONFLICT 984 985 KT -> NS (IN REF. 1).

CC -!- SQ SEQUENCE 1064 AA; 120070 MW; E4104B84A8E45C36 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 1064;
 Best Local Similarity 50.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YMRFVYPTKTFP 12
 Db 802 YMRFPMPSAYP 813

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:46:48 ; search time 42.51 Seconds
(without alignments)
40.460 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
76 1 YMRFVYPTKTEPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rabbit:*
12: sp_unclassified:*
13: sp_vertetebrate:*
14: sp_virus:*

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ALIGNMENTS

RESULT	1
ID	Q9R1E6
AC	Q9R1E6;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (EC 3.1.4.1).
GN	NPPS2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA	Sano K.; Piao J.-H.;
RT	"Cloning and chromosomal assignment of mouse phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha'autotaxin).";
RL	Submitted (JAN-1999) to the EMBL/GenBank/DDJB databases.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6;
RA	
RT	
RL	
DR	InterPro; IPR001212; -.
DR	InterPro; IPR002591; -.
DR	Pfam; PF01033; Somatomedin_B; 2.
DR	Pfam; PF01663; Phosphodiest; 1.
DR	PRINTS; PR00022; SOMATOMEDINB.
DR	PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR	SMART; SM00201; SO; 1.
KW	Hydrolase.
SQ	SEQUENCE 862 AA; 98918 MW; 641F8F1443E4F8B0 CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	76	100.0	862	11	Q9R1E6		Q9r1e6 mus musculus
2	76	100.0	863	4	Q13822		Q13822 homo sapien
3	76	100.0	863	4	Q15117		Q15117 homo sapien
4	76	100.0	915	4	Q13827		Q13827 homo sapien
5	70	92.1	885	11	Q64610		Q64610 rattus norvegicus
6	69	90.8	257	11	Q88827		Q88827 rattus norvegicus
7	69	90.8	845	4	Q9NPZ3		Q9npz3 homo sapien
8	69	90.8	925	4	Q9P1P6		Q9p1p6 homo sapien
9	68	89.5	875	11	P97675		P97675 rattus norvegicus
10	68	89.5	876	11	P70641		P70641 rattus norvegicus
11	65	85.5	875	4	O14638		O14638 homo sapien
12	65	85.5	875	11	Q63490		Q63490 rattus norvegicus
13	65	85.5	875	11	P97676		P97676 rattus norvegicus
14	64	84.2	32	6	Q9TRD2		Q9trd2 bos taurus
15	64	84.2	817	14	O90761		O90761 fowlpox virus
16	64	84.2	817	14	O9J5H1		O9j5h1 fowlpox virus
17	49	64.5	457	10	Q9SU82		Q9su82 arabidopsis
18	49	64.5	461	10	Q9SU81		Q9su81 arabidopsis
19	49	64.5	829	5	P90754		P90754 caenorhabditis

Query Match 100.0%; Score 76; DB 11; Length 862;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 13; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

QY 1 YMRFVYPTKTEPN 13
Db 200 YMRFVYPTKTEPN 212

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Q13822; [1]	SEQUENCE FROM N.A.		
DC TISSUE=TESTIS;			
DC MEDLINE=95074054; PubMed=7982964;			
DR RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,			
DR RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
RN [2]	SEQUENCE FROM N.A.		
RC TISSUE=TESTIS;			
RX MEDLINE=96158950; PubMed=8579579;			
RA Lee H.Y., Murata J., Clair T., Polymeropoulos M.H., Torres R.,			
RA Manrow R.E., Liotta L.A., Stracke M.L.;			
RT "Cloning, chromosomal localization, and tissue expression of autotaxin from human teratocarcinoma cells";			
RT Biochem. Biophys. Res. Commun. 218:714-719(1996).			
RL EMBL; L46720; AAB0855.1; -.			
DR InterPro; IPR001212; -.			
DR InterPro; IPR001604; -.			
DR InterPro; IPR002591; -.			
DR Pfam; PF01033; Somatomedin_B; 2.			
DR Pfam; PF01663; Phosphodiest; 1.			
DR PRINTS; PRO0022; SOMATOMEDINB.			
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.			
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SQ SEQUENCE 863 AA; 99017 MW; F960DCE51663BAB CRC64;			
RN [1]	SEQUENCE FROM N.A.		
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RX MEDLINE=95074054; PubMed=7982964;			
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,			
RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
DR InterPro; IPR001212;			
DR InterPro; IPR001604;			
DR InterPro; IPR002591;			
DR Pfam; PF01033; Somatomedin_B; 2.			
DR Pfam; PF01663; Phosphodiest; 1.			
DR PRINTS; PRO0022; SOMATOMEDINB.			
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DR SMART; SM00477; NUC; 1.			
SQ SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;			
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RC TISSUE=TUMOR;			
RX MEDLINE=95074054; PubMed=7982964;			
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,			
RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
DR InterPro; IPR001212;			
DR InterPro; IPR001604;			
DR InterPro; IPR002591;			
DR Pfam; PF01033; Somatomedin_B; 2.			
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DR PRINTS; PRO0022; SOMATOMEDINB.			
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RN [1]	SEQUENCE FROM N.A.		
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RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
DR InterPro; IPR001212;			
DR InterPro; IPR001604;			
DR InterPro; IPR002591;			
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RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
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DR InterPro; IPR002591;			
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DR PRINTS; PRO0022; SOMATOMEDINB.			
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RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,			
RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
DR InterPro; IPR001212;			
DR InterPro; IPR001604;			
DR InterPro; IPR002591;			
DR Pfam; PF01033; Somatomedin_B; 2.			
DR Pfam; PF01663; Phosphodiest; 1.			
DR PRINTS; PRO0022; SOMATOMEDINB.			
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RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
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DR InterPro; IPR002591;			
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RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
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DR InterPro; IPR002591;			
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RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
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DR InterPro; IPR001604;			
DR InterPro; IPR002591;			
DR Pfam; PF01033; Somatomedin_B; 2.			
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DR PRINTS; PRO0022; SOMATOMEDINB.			
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.			
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RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,			
RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol. Chem. 269:30479-30484(1994).			
DR EMBL; L35594; AAA64785.1; -.			
DR InterPro; IPR001212;			
DR InterPro; IPR001604;			
DR InterPro; IPR002591;			
DR Pfam; PF01033; Somatomedin_B; 2.			
DR Pfam; PF01663; Phosphodiest; 1.			
DR PRINTS; PRO0022; SOMATOMEDINB.			
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.			
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RC TISSUE=TUMOR;			
RX MEDLINE=95074054; PubMed=7982964;			
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,			
RA Sobel M.E., Liotta L.A., Stracke M.L.;			
RT "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases.";			
RL J. Biol			

OX NCBI_TAXID=10116;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=95050605; PubMed=7961762;
 RA Narita M., Goji J., Nakamura H., Sano K.;
 RT "Molecular cloning, expression, and localization of a brain-specific phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha) from rat brain.";
 RT PROSITE; PS00524; SOMATOMEDIN_B; 2.
 RL J. Biol. Chem. 269:28235-28242(1994).
 DR EMBL; D28560; BAA5910..1; -.
 DR InterPro; IPR001212; -.
 DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR Pfam; PF01663; Phosphodiest; 1.
 DR PRINTS; PR00022; SOMATOMEDINB.
 DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
 DR SMART; SM00477; NUC; 1.
 KW Hydrolase.
 SQ SEQUENCE 885 AA; 101309 MW; BC5C0AFC52007973 CRC64;

Query Match 92.1%; Score 70; DB 11; Length 885;
 Best Local Similarity 92.3%; Pred. No. 0.00065;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 Db 198 YTRPVYPTKTFPN 210

RESULT 6
 ID 088827 PRELIMINARY;
 AC 088827;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PLASMA CELL MEMBRANE GLYCOPROTEIN (FRAGMENT).
 GN PC1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sakoda H., Asano T., Ogihara T.;
 RT "N terminal of the plasma cell membrane glycoprotein PC-1.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB017596; BAA33393..1; -.
 DR InterPro; IPR001212; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR PRINTS; PR00022; SOMATOMEDINB.
 DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
 DR SMART; SM00201; SO; 1.
 FT NON_TER 257
 SQ SEQUENCE 257 AA; 28306 MW; CF348E474FBDAFED CRC64;

Query Match 90.8%; Score 69; DB 11; Length 257;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
 Db 230 MRPVYPTKTFPN 241

RESULT 7
 Q9NPZ3 PRELIMINARY;
 ID Q9NPZ3 PRT; 845 AA.
 AC Q9NPZ3;

DR EMBL; AFI10301; AAF36094.1; JOINED.
 DR EMBL; AFI10302; AAF36094.1; JOINED.
 DR EMBL; AFI10303; AAF36094.1; JOINED.
 DR InterPro; IPR001212; -.
 DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR Pfam; PF01663; Phosphodiest; 1.
 DR PRINTS; PR00022; SOMATOMEDINB; 2.
 DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
 DR SMART; SM00477; NUC; 1.
 SEQUENCE 925 AA; 104924 MW; 0ECAA063801CAFE8 CRC64;

Query Match 90.8%; Score 69; DB 4; Length 925;
 Best Local Similarity 100.0%; Pred. No. 0.001; Gaps 0;
 Matches 12; Conservative 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
 Db 248 MRPVYPTKTFPN 259

RESULT 9
 P97675 PRELIMINARY; PRT; 875 AA.
 ID P97675; AC P97675; DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ALKALINE PHOSPHODIESTERASE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116; RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=97250927; PubMed=9096610;
 RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W., Maurice M.;
 RA "Biochemical and molecular identification of distinct forms of RT alkaline phosphodiesterase I expressed on the apical and basolateral RT plasma membrane surfaces of rat hepatocytes.";
 RL Hepatology 25:995-1002(1997).
 EMBL; U78787; AAB61535.1; -.
 DR InterPro; IPR001212; -.
 DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR Pfam; PF01663; Phosphodiest; 1.
 DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
 DR SMART; SM00477; NUC; 1.
 SEQUENCE 875 AA; 99166 MW; 8FEB9A482173D377 CRC64;

Query Match 89.5%; Score 68; DB 11; Length 875;
 Best Local Similarity 92.3%; Pred. No. 0.0014; Gaps 0;
 Matches 12; Conservative 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 Db 197 YMRAVYPTKTFPN 209

RESULT 10
 P70641 ID P70641 PRELIMINARY; PRT; 876 AA.
 AC P70641; DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE PHOSPHODIESTERASE I.

DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR Pfam; PF01663; Phosphodiest; 1.
 DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
 DR SMART; SM00477; NUC; 1.
 DR Hydrolase.
 KW SEQUENCE 875 AA; 100096 MW; 329CF41667497BC4 CRC64;
 SQ

Query Match 85.5%; Score 65; DB 4; Length 875;
 Best Local Similarity 84.6%; Pred. No. 0.0048;
 Matches 11; Conservative 1; Indels 0; Gaps 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
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 Db 196 YMRAMYPTKTFPN 208

RESULT 12
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 ID Q63490
 AC Q63490;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE RB13-6 ANTIGEN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAQUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=9524775; PubMed=7730366;
 RA Deissler H., Lottspeich F., Rajewsky M.F.;
 RT "Affinity purification and cDNA cloning of rat neural differentiation
 and tumor cell surface antigen gp130RB13-6 reveals relationship to
 human and murine PC-1."
 RT RL Biol. Chem. 270:9849-9855(1995).
 DR EMBL; Z47987; CAA88029; 1; -.
 DR InterPro; IPR001212; -.
 DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR Pfam; PF01663; Phosphodiest; 1.
 DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
 DR SMART; SM00477; NUC; 1.
 SQ SEQUENCE 875 AA; 99087 MW; 9BA9FBFEF82DFFB46 CRC64;

Query Match 85.5%; Score 65; DB 11; Length 875;
 Best Local Similarity 84.6%; Pred. No. 0.0048;
 Matches 11; Conservative 1; Indels 0; Gaps 0;

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 Db 197 YMRAMYPTKTFPN 209

RESULT 13
 P97676 PRELIMINARY; PRT; 875 AA.
 ID P97676
 AC P97676;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ALKALINE PHOSPHODIESTERASE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

Query Match 85.5%; Score 65; DB 11; Length 875;
 Best Local Similarity 84.6%; Pred. No. 0.0048;
 Matches 11; Conservative 1; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 ||| :|||||||
 Db 197 YMRAMYPTKTFPN 209

RESULT 14
 Q9TRD2 PRELIMINARY; PRT; 32 AA.
 ID Q9TRD2
 AC Q9TRD2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE 260 KDa MAJOR ACIDIC FIBROBLAST GROWTH FACTOR-STIMULATED
 DE PHOSPHOPROTEIN (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94086550; PubMed=7505270;
 RA Oda Y., Kuo M.D., Huang S.S., Huang J.S.;
 RT "The major acidic fibroblast growth factor (aFGF)-stimulated
 phosphoprotein from bovine liver plasma membranes has aFGF-stimulated
 kinase, autoadenylation, and alkaline nucleotide phosphodiesterase
 activities."
 RT RL J. Biol. Chem. 268:27318-27326(1993).
 SQ SEQUENCE 32 AA; 3699 MW; 5CCFFA9EB55E6927 CRC64;

Query Match 84.2%; Score 64; DB 6; Length 32;
 Best Local Similarity 91.7%; Pred. No. 0.0002;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MRPVYPTKTFPN 13
 ||| :|||||||
 Db 2 MRPVYPTKTFPN 13

RESULT 15
 O90761 PRELIMINARY; PRT; 817 AA.
 ID O90761
 AC O90761;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE)
 DE NUCLEOTIDE PHOSPHODIESTERASE.
 GN PCL.
 OS Fowlpox virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OC NCBI_TaxID=10261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FP-9;
 RX MEDLINE=98325194; PubMed=9658122;
 RA Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;
 RT "fowlpox virus encodes nonessential homologs of cellular alpha-SNAP,
 PC-1, and an orphan human homolog of a secreted nematode protein.";
 RL J. Virol. 72:6742-6751(1998).
 CC -i- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 DR EMBL; AJ006408; CAA07014.1; - .
 DR InterPro; IPR001604; - .
 DR InterPro; IPR002591; - .
 DR Pfam; PF01663; Phosphodiest; 1.
 DR SMART; SM00477; NUC; 1.
 KW Hydrolase.
 SQ SEQUENCE 817 AA; 94004 MW; CB68DA0508CC568E CRC64;

Query	Match	Score	DB	Length	Indels	Gaps	O;
Best Local Matches	Similarity 91.7%; Conservative 11;	84.2%	14	817	0	0	
QY	2 MRPVYPTKTFPN 13						
Db	155 MRPVYPTNTFPN 166						

Search completed: July 19, 2001, 14:46:49
 Job time: 172 sec